

1/498

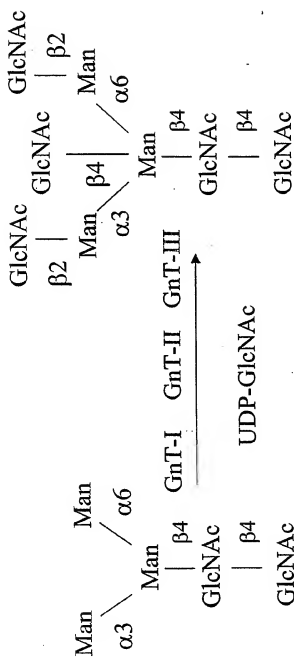
Trimannosyl core with  
Bisecting GlcNAc

FIG. 1

Trimannosyl core

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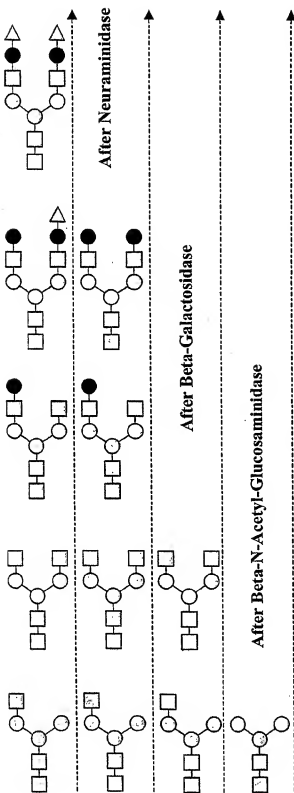
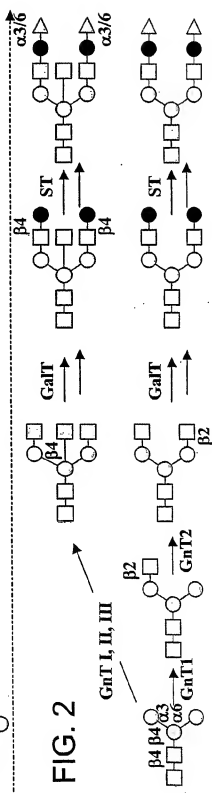


FIG. 2



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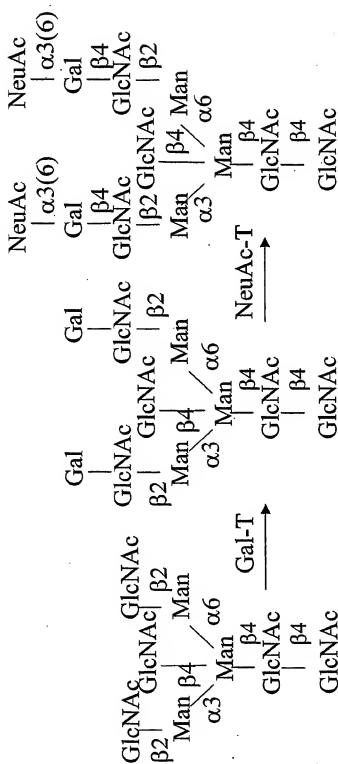


FIG. 3

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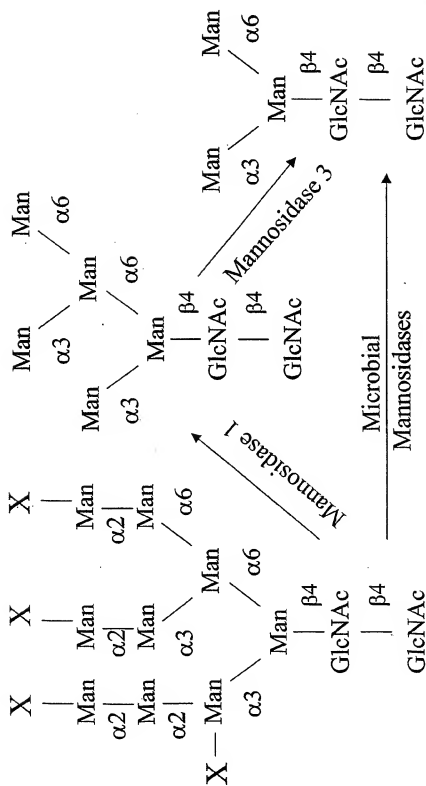


FIG. 4



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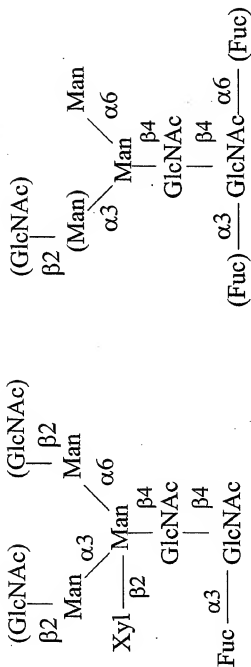


FIG. 5

FIG. 6



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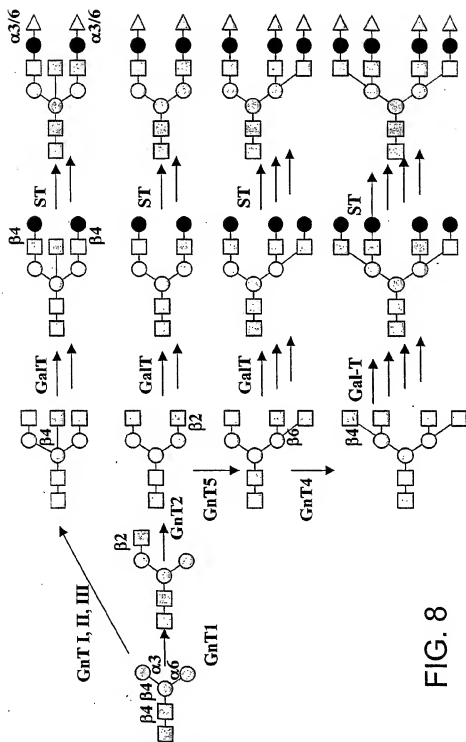


FIG. 8

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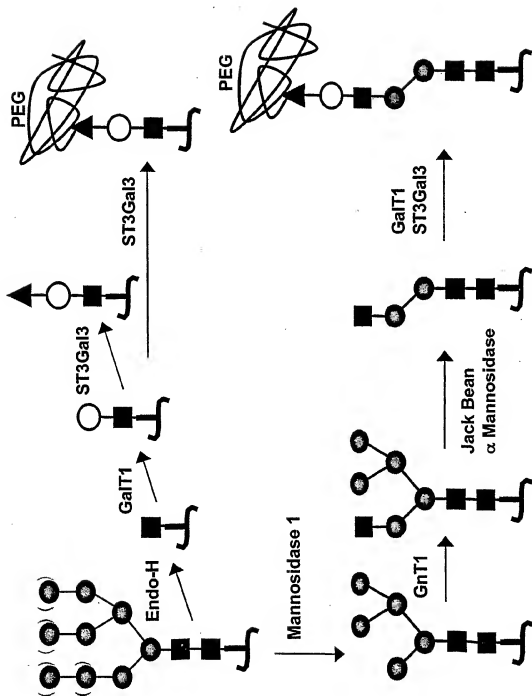


FIG. 9

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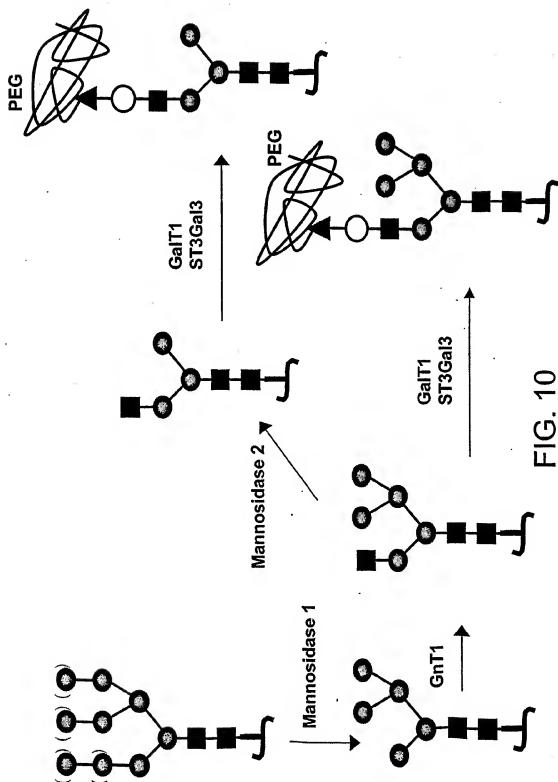


FIG. 10

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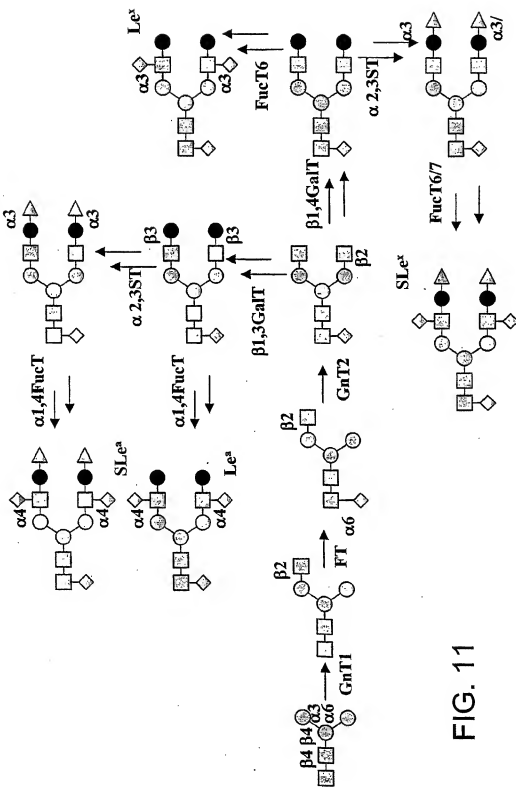


FIG. 11

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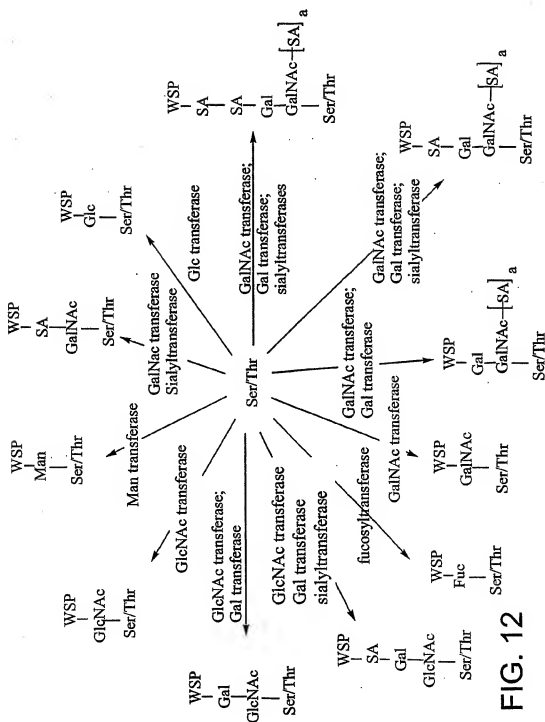


FIG. 12

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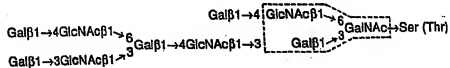
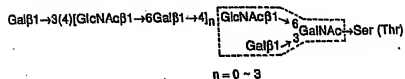
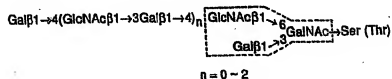
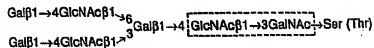
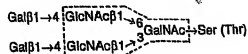
**Core 1****Core 2****Core 3****Core 4**

FIG. 13





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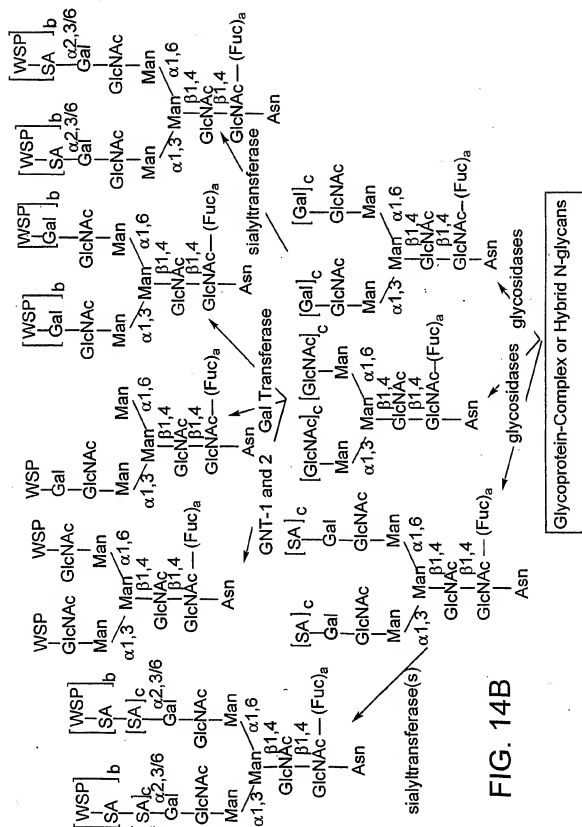


FIG. 14B

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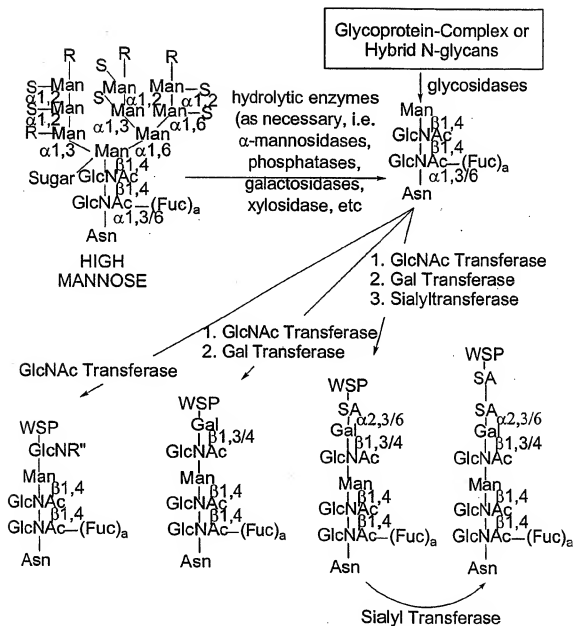


FIG. 15



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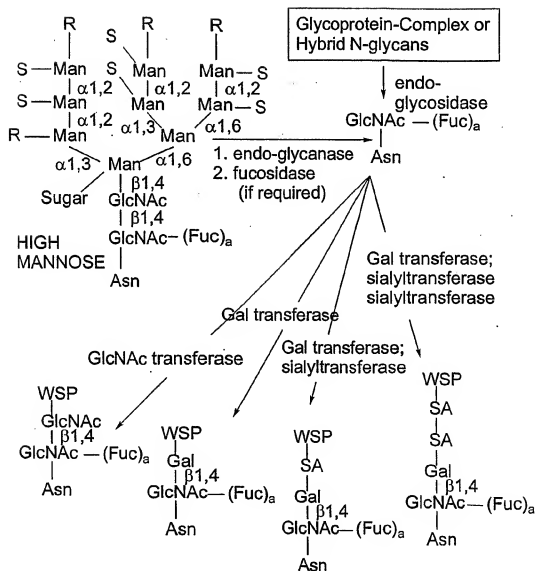


FIG. 17











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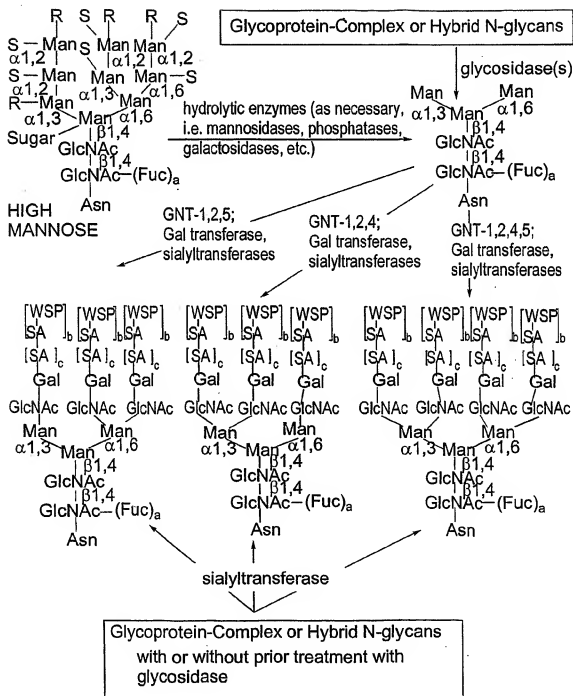
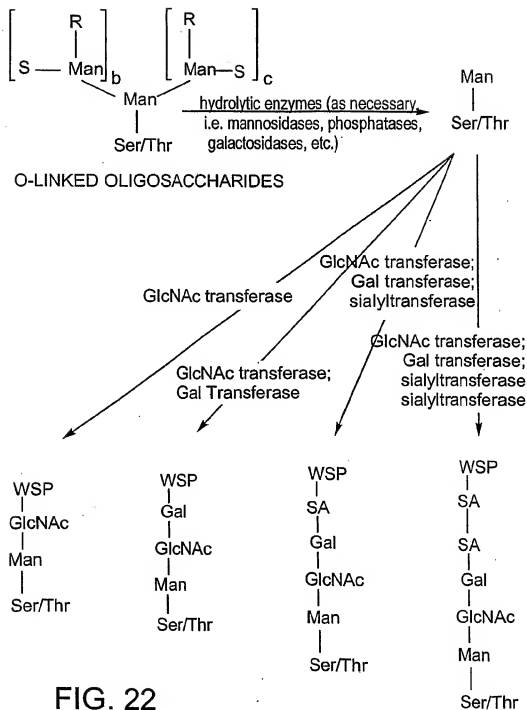


FIG. 20



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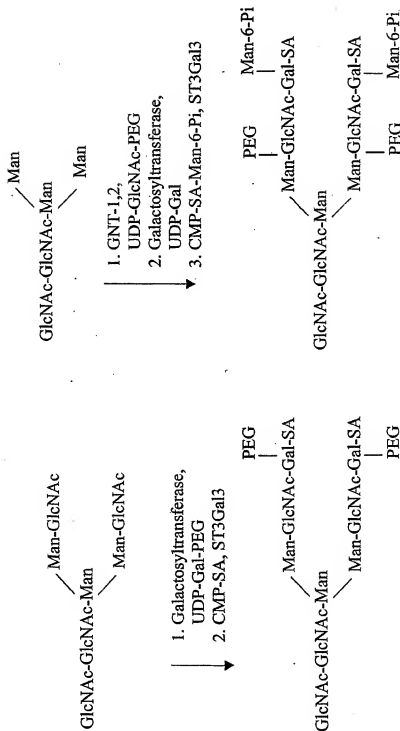


FIG. 23A

FIG. 23B

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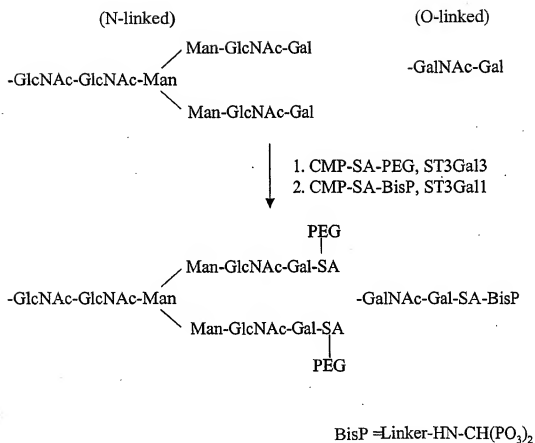


FIG. 23C

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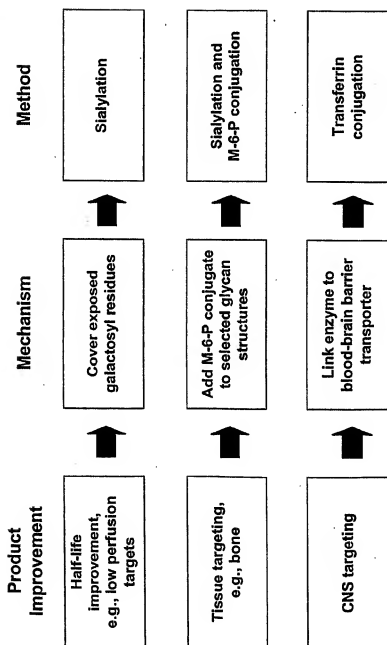


FIG. 24

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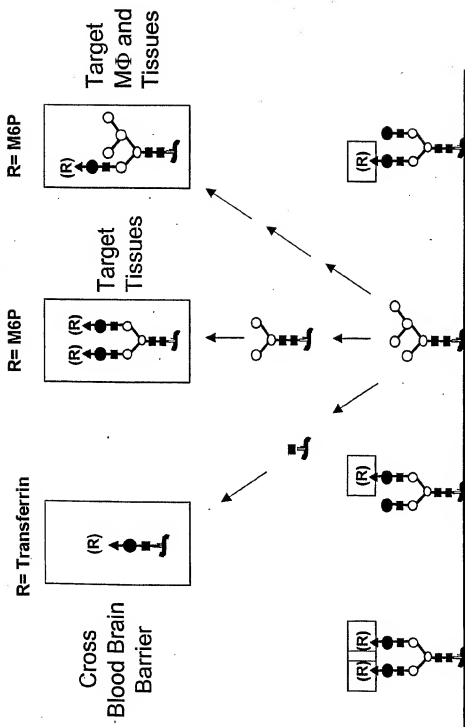


FIG. 25



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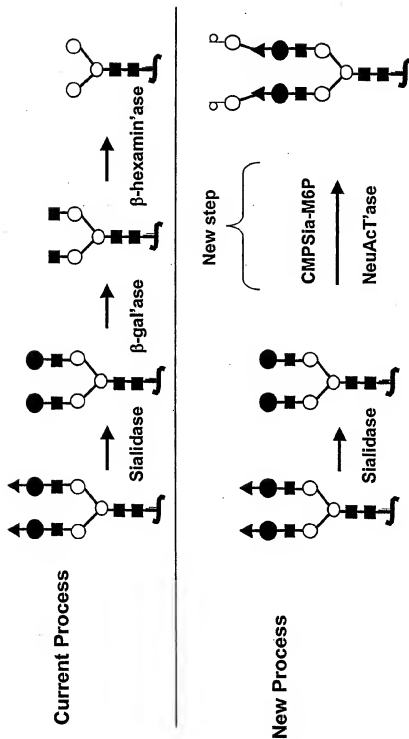


FIG. 26

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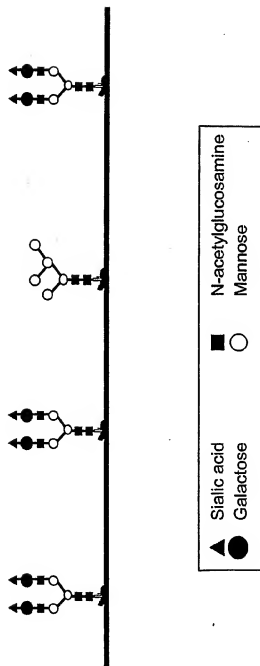


FIG. 27

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12AP1/E5 -- Viventia Biotech  
 1964 -- Aventis  
 20K growth hormone -- AMUR  
 28P6/E6 -- Viventia Biotech  
 3-Hydroxyphthaloyl-beta-lactoglobulin --  
 4-IBB ligand gene therapy --  
 64-Cu MAb conjugate TETA-1A3 --  
 Mallinckrodt Institute of Radiology  
 64-Cu MAb conjugate TETA-cT84.66  
 64-Cu Trastuzumab TETA conjugate --  
 Genentech  
 A 200 -- Amgen  
 A10255 -- Eli Lilly  
 A1PDX -- Hedral Therapeutics  
 A6 -- Angstrom  
 aaAT-III -- Genzyme  
 Abciximab -- Centocor  
 ABI.001 -- Atlantic BioPharmaceuticals  
 ABT-828 -- Abbott  
 Accutin  
 Actinohivin  
 activin -- Biotech Australia, Human  
 Therapeutics, Curis  
 AD 439 -- Tanox  
 AD 519 -- Tanox  
 Adalimumab -- Cambridge Antibody Tech.  
 Adenocarcinoma vaccine -- Biomira -- NIS  
 Adenosine deaminase -- Enzon  
 Adenosine A2B receptor antagonists --  
 Adenosine Therapeutics  
 ADP-001 -- Axis Genetics  
 AF 13948 -- Affymax  
 Afelimomab -- Knoll  
 AFP-SCAN -- Immunomedics  
 AG 2195 -- Corixa  
 agalsidase alfa -- Transkaryotic Therapies  
 agalsidase beta -- Genzyme  
 AGENT-- Antisoma  
 AI 300 -- Autolimmune  
 AI-101 -- Teva  
 AI-102 -- Teva  
 AI-201 -- Autolimmune  
 AI-301 -- Autolimmune  
 AIDS vaccine -- ANRS, CIBG, Hese  
 Biomed, Hollis-Eden, Rome, United  
 Biomedical, American Home Products,  
 Maxygen  
 airway receptor ligand -- IC Innovations  
 AJW 2 -- Ajinomoto  
 AK 30 NGF -- Alkermes  
 Albuferon -- Human Genome Sciences  
 albumin -- Biogen, DSM Anti-Infectives,  
 Genzyme Transgenics, PPL Therapeutics,  
 TranXenoGen, Welfide Corp.  
 aldesleukin -- Chiron  
 alefacept -- Biogen  
 Alemtuzumab  
 Allergy therapy -- ALK-Abello/Maxygen,  
 ALK-Abello/RP Scherer  
 allergy vaccines -- Allergy Therapeutics  
 Alnidofibatide -- Aventis Pasteur  
 Alnorine -- SRC VB VECTOR  
 ALP 242 -- Gruenenthal  
 Alpha antitrypsin -- Arriva/Hyaland  
 Immuno/ProMetic/Protease Sciences  
 Alpha-1 antitrypsin -- Cutter, Bayer, PPL  
 Therapeutics, Profile, ZymoGenetics,  
 Arriva  
 Alpha-1 protease inhibitor -- Genzyme  
 Transgenics, Welfide Corp.  
 Alpha-galactose fusion protein --  
 Immunomedics  
 Alpha-galactosidase A -- Research  
 Corporation Technologies, Genzyme  
 Alpha-glucosidase -- Genzyme, Novazyme  
 Alpha-lactalbumin  
 Alpha-L-iduronidase -- Transkaryotic  
 Therapies, BioMarin  
 alteplase -- Genentech  
 alvircept sudotox -- NIH  
 ALX-0600, a GLP-2 agonist -- NPS Allelix  
 Corp.

FIG. 28A

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ALX1-11 --sNPS Pharmaceuticals  
 Alzheimer's disease gene therapy  
 AM-133 -- AMRAD  
 Amb a 1 immunostim conj. -- Dynavax  
 AMD 3100 -- AnorMED -- NIS  
 AMD 3465 -- AnorMED -- NIS  
 AMD 3465 -- AnorMED -- NIS  
 AMD Fab -- Genentech  
 Amediplase -- Menarini, Novartis  
 AM-F9  
 Amoebiasis vaccine  
 Amphiregulin -- Octagene  
 anakinra -- Amgen  
 analgesic -- Nobex  
 aneastim -- Amgen  
 Anergix.RA -- Corixa, Organon  
 Angiocidin -- InKine  
 angiogenesis inhibitors -- ILEX  
 AngioMab -- Antisoma  
 Angiopoietins -- Regeneron/Procter &  
 Gamble  
 angiostatin -- EntreMed  
 Angiostatin/endostatin gene therapy --  
 Genetix Pharmaceuticals  
 angiotensin-II, topical -- Maret  
 Anthrax -- EluSys Therapeutics/US Army  
 Medical Research Institute  
 Anthrax vaccine  
 Anti platelet-derived growth factor D human  
 monoclonal antibodies -- CuraGen  
 Anti-17-1A Mab 3622W94 --  
 GlaxoSmithKline  
 Anti-2C4 Mab -- Genentech  
 anti-4-1BB monoclonal antibodies -- Bristol-  
 Myers Squibb  
 Anti-Adhesion Platform Tech. -- CytoVax  
 Anti-adipocyte Mab -- Cambridge Antibody  
 Tech./ObeSys  
 antiallergics -- Maxygen  
 antiallergy vaccine -- Acambis  
 Anti-alpha-4-integrin Mab  
 Anti-alphavβ3 integrin Mab -- Applied  
 Molecular Evolution  
 Anti-angiogenesis monoclonal antibodies --  
 KS Biomedix/Schering AG  
 Anti-B4 Mab-DC1 conjugate -- ImmunoGen  
 Anti-B7 antibody PRIMATIZED -- IDEC  
 Anti-B7-1 Mab 16-10A1  
 Anti-B7-1 Mab 1G10  
 Anti-B7-2 Mab GL-1  
 Anti-B7-2-gelonin immunotoxin --  
 Antibacterials/antifungals --  
 Diversa/IntraBiotics  
 Anti-beta-amyloid monoclonal antibodies --  
 Cambridge Antibody Tech., Wyeth-Ayerst  
 Anti-BLyS antibodies -- Cambridge  
 Antibody Tech./Human Genome Sciences  
 Antibody-drug conjugates -- Seattle  
 Genetics/Eos  
 Anti-C5 Mab BB5-1 -- Alexion  
 Anti-C5 Mab N19-8 -- Alexion  
 Anti-C8 Mab  
 anticancer cytokines -- BioPulse  
 anticancer matrix -- Telios Integra  
 Anticancer monoclonal antibodies -- ARIUS,  
 Immunex  
 anticancer peptides -- Maxygen, Micrologix  
 Anticancer prodrug Tech. -- Alexion  
 Antibody Technologies  
 anticancer Troy-Bodies -- Affite -- Affitech  
 anticancer vaccine -- NIH  
 anticancers -- Epimmune  
 Anti-CCR5/CXCR4 sheep Mab -- KS  
 Biomedix Holdings  
 Anti-CD11a Mab KBA --  
 Anti-CD11a Mab M17  
 Anti-CD11a Mab TA-3 --  
 Anti-CD11a Mab WT.1 --  
 Anti-CD11b Mab -- Pharmacia  
 Anti-CD11b Mab LM2  
 Anti-CD154 Mab -- Biogen  
 Anti-CD16-anti-CD30 Mab -- Biotest

FIG. 28B

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Anti-CD18 MAb -- Pharmacia	Anti-CD4 MAb -- Centocor, IDEC
Anti-CD19 MAb B43 --	Pharmaceuticals, Xenova Group
Anti-CD19 MAb -liposomal sodium butyrate conjugate --	Anti-CD4 MAb 16H5
Anti-CD147	Anti-CD4 MAb 4162W94 -- GlaxoSmithKline
Anti-CD19 MAb-saporin conjugate --	Anti-CD4 MAb B-F5 -- Diaclone
Anti-CD19-dsFv-PE38-immunotoxin --	Anti-CD4 MAb GK1-5
Anti-CD2 MAb 12-15 --	Anti-CD4 MAb KT6
Anti-CD2 MAb B-E2 -- Diaclone	Anti-CD4 MAb OX38
Anti-CD2 MAb OX34 --	Anti-CD4 MAb PAP conjugate -- Bristol-Myers Squibb
Anti-CD2 MAb OX54 --	Anti-CD4 MAb RIB 5-2
Anti-CD2 MAb OX55 --	Anti-CD4 MAb W3/25
Anti-CD2 MAb RM2-1	Anti-CD4 MAb YTA 3.1.2
Anti-CD2 MAb RM2-2	Anti-CD4 MAb YTS 177-9
Anti-CD2 MAb RM2-4	Anti-CD40 ligand MAb 5c8 -- Biogen
Anti-CD20 MAb BCA B20	Anti-CD40 MAb
Anti-CD20-anti-Fc alpha RI bispecific MAb -- Medarex, Tenovus	Anti-CD40 MAb 5D12 -- Tanox
Anti-CD22 MAb-saporin-6 complex --	Anti-CD44 MAb A3D8
Anti-CD3 Immunotoxin --	Anti-CD44 MAb GKWA3
Anti-CD3 MAb 145-2C11 -- Pharming	Anti-CD44 MAb IM7
Anti-CD3 MAb CD4IgG conjugate -- Genentech	Anti-CD44 MAb KM81
Anti-CD3 MAb humanised -- Protein Design, RW Johnson	Anti-CD44 variant monoclonal antibodies -- Corixa/Hebrew University
Anti-CD3 MAb WT32	Anti-CD45 MAb BC8-I-131
Anti-CD3 MAb-ricin-chain-A conjugate --	Anti-CD45RB MAb
Anti-CD3 MAb-xanthine-oxidase conjugate --	Anti-CD48 MAb HuLy-m3
Anti-CD30 MAb BerH2 -- Medac	Anti-CD48 MAb WM-63
Anti-CD30 MAb-saporin conjugate	Anti-CD5 MAb -- Becton Dickinson
Anti-CD30-scFv-ETA'-immunotoxin	Anti-CD5 MAb OX19
Anti-CD38 MAb AT13/5	Anti-CD6 MAb
Anti-CD38 MAb-saporin conjugate	Anti-CD7 MAb-PAP conjugate
Anti-CD3-anti-CD19 bispecific MAb	Anti-CD7 MAb-ricin-chain-A conjugate
Anti-CD3-anti-EGFR MAb	Anti-CD8 MAb -- Amerimmune, Cytodyn, Becton Dickinson
Anti-CD3-anti-interleukin-2-receptor MAb	Anti-CD8 MAb 2-43
Anti-CD3-anti-MOV18 MAb -- Centocor	Anti-CD8 MAb OX8
Anti-CD3-anti-SCLC bispecific MAb	Anti-CD80 MAb P16C10 -- IDEC
Anti-CD4 idiotype vaccine	Anti-CD80 MAb P7C10 -- ID Vaccine
	Anti-CD8-idarubicin conjugate
	Anti-CEA MAb CE-25
	Anti-CEA MAb MN 14 -- Immunomedics

FIG. 28C

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- Anti-CEA MAb MN14-PE40 conjugate -- Immunomedics
- Anti-CEA MAb T84.66-interleukin-2 conjugate
- Anti-CEA sheep MAb -- KS Biomedix Holdings
- Anti-cell surface monoclonal antibodies -- Cambridge Antibody Tech. /Pharmacia
- Anti-c-erbB2-anti-CD3 bifunctional MAb -- Otsuka
- Anti-CMV MAb -- Scotgen
- Anti-complement
- Anti-CTLA-4 MAb
- Anti-EGFR catalytic antibody -- Hersed Biomed
- anti-EGFR immunotoxin -- IVAX
- Anti-EGFR MAb -- Abgenix
- Anti-EGFR MAb 528
- Anti-EGFR MAb KSB 107 -- KS Biomedix
- Anti-EGFR MAb-DM1 conjugate -- ImmunoGen
- Anti-EGFR MAb-LA1 --
- Anti-EGFR sheep MAb -- KS Biomedix
- Anti-FAP MAb F19-I-131
- Anti-Fas IgM MAb CH11
- Anti-Fas MAb Jo2
- Anti-Fas MAb RK-8
- Anti-Fit-1 monoclonal antibodies -- ImClone
- Anti-fungal peptides -- State University of New York
- antifungal tripeptides -- BTG
- Anti-ganglioside GD2 antibody-interleukin-2 fusion protein -- Lexigen
- Anti-GM2 MAb -- Kyowa
- Anti-GM-CSF receptor monoclonal antibodies -- AMRAD
- Anti-gp130 MAb -- Tosoh
- Anti-HCA monoclonal antibodies -- AltaRex/Epigen
- Anti-hCG antibodies -- Abgenix/AVI BioPharma
- Anti-heparanase human monoclonal antibodies -- Oxford Glycosciences/Medarex
- Anti-hepatitis C virus human monoclonal antibodies -- XTL Biopharmaceuticals
- Anti-HER-2 antibody gene therapy
- Anti-herpes antibody -- Epicyte
- Anti-HIV antibody -- Epicyte
- anti-HIV catalytic antibody -- Hersed Biomed
- anti-HIV fusion protein -- Idun
- anti-HIV proteins -- Cangene
- Anti-HM1-24 MAb -- Chugai
- Anti-hrR3 MAb
- Anti-Human-Carcinoma-Antigen MAb -- Epicyte
- Anti-ICAM-1 MAb -- Boehringer Ingelheim
- Anti-ICAM-1 MAb 1A-29 -- Pharmacia
- Anti-ICAM-1 MAb HA58
- Anti-ICAM-1 MAb YN1/1.7.4
- Anti-ICAM-3 MAb ICM3 -- ICOS
- Anti-idiotypic breast cancer vaccine 11D10
- Anti-idiotypic breast cancer vaccine ACA14C5 --
- Anti-idiotypic cancer vaccine -- ImClone Systems/Merck KGaA ImClone, Viventia Biotech
- Anti-idiotypic cancer vaccine 1A7 -- Titan
- Anti-idiotypic cancer vaccine 3H1 -- Titan
- Anti-idiotypic cancer vaccine TriAb -- Titan
- Anti-idiotypic Chlamydia trachomatis vaccine
- Anti-idiotypic colorectal cancer vaccine -- Novartis
- Anti-idiotypic colorectal cancer vaccine -- Onyvox
- Anti-idiotypic melanoma vaccine -- IDEC Pharmaceuticals
- Anti-idiotypic ovarian cancer vaccine ACA 125
- Anti-idiotypic ovarian cancer vaccine AR54 - AltaRex

FIG. 28D

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Anti-idiotype ovarian cancer vaccine CA-125 – AltaRex, Biomira	Anti-L-selectin monoclonal antibodies -- Protein Design Labs, Abgenix, Stanford University
Anti-IgE catalytic antibody -- Hesed Biomed	Anti-MBL monoclonal antibodies -- Alexion/Brigham and Women's Hospital
Anti-IgE MAb E26 -- Genentech	Anti-MHC monoclonal antibodies
Anti-IGF-1 MAb	Anti-MIF antibody humanised -- IDEC, Cytokine PharmaSciences
anti-inflammatory -- GeneMax	Anti-MRSA/VRSA sheep MAb -- KS Biomedix Holdings
anti-inflammatory peptide -- BTG	Anti-mu MAb -- Novartis
anti-integrin peptides -- Burnha	Anti-MUC-1 MAb
Anti-interferon-alpha-receptor MAb 64G12 -- Pharma Pacific Management	Anti-MUC 18
Anti-interferon-gamma MAb -- Protein Design Labs	Anti-Nogo-A MAb IN1
Anti-interferon-gamma polyclonal antibody - Advanced Biotherapy	Anti-nuclear autoantibodies -- Procyon
Anti-interleukin-10 MAb --	Anti-ovarian cancer monoclonal antibodies -
Anti-interleukin-12 MAb --	- Dompe
Anti-interleukin-1-beta polyclonal antibody -- R&D Systems	Anti-p185 monoclonal antibodies
Anti-interleukin-2 receptor MAb 2A3	Anti-p43 MAb
Anti-interleukin-2 receptor MAb 33B3-1 -- Immunotech	Antiparasitic vaccines
Anti-interleukin-2 receptor MAb ART-18	Anti-PDGF/bFGF sheep MAb -- KS Biomedix
Anti-interleukin-2 receptor MAb LO-Tact-1	Anti-properdin monoclonal antibodies -- Abgenix/Gliatech
Anti-interleukin-2 receptor MAb Mikbeta1	Anti-PSMA (prostrate specific membrane antigen)
Anti-interleukin-2 receptor MAb NDS61	Anti-PSMA MAb J591 -- BZL Biologics
Anti-interleukin-4 MAb 11B11	Anti-Rev MAb gene therapy --
Anti-interleukin-5 MAb -- Wallace Laboratories	Anti-RSV antibodies -- Epicyte, Intracell
Anti-interleukin-6 MAb -- Centocor, Diacorne, Pharmadigm	Anti-RSV monoclonal antibodies -- Medarex/MedImmune, Applied Molecular Evolution/MedImmune
Anti-interleukin-8 MAb -- Abgenix	Anti-RSV MAb, inhalation -- Alkermes/MedImmune
Anti-interleukin-8 MAb -- Xenotech	Anti-RT gene therapy
Anti-JL1 MAb	Antisense K-ras RNA gene therapy
Anti-Klebsiella sheep MAb -- KS Biomedix Holdings	Anti-SF-25 MAb
Anti-Laminin receptor MAb-liposomal doxorubicin conjugate	Anti-sperm antibody -- Epicyte
Anti-LCG MAb -- Cytoclonal	Anti-Tac(Fv)-PE38 conjugate
Anti-lipopolysaccharide MAb -- VitaResc	Anti-TAPA/CD81 MAb AMP1
	Anti-tat gene therapy

FIG. 28E

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Anti-TCR-alphabeta MAb H57-597  
 Anti-TCR-alphabeta MAb R73  
 Anti-tenascin MAb BC-4-I-131  
 Anti-TGF-beta human monoclonal  
   antibodies -- Cambridge Antibody Tech.,  
   Genzyme  
 Anti-TGF-beta MAb 2G7 -- Genentech  
 Antithrombin III -- Genzyme Transgenics,  
   Aventis, Bayer, Behringwerke, CSL,  
   Myriad  
 Anti-Thy1 MAb  
 Anti-Thy1.1 MAb  
 Anti-tissue factor/factor VIIA sheep MAb --  
   KS Biomedix  
 Anti-TNF monoclonal antibodies --  
   Centocor, Chiron, Peptech, Pharacia,  
   Serono  
 Anti-TNF sheep MAb -- KS Biomedix  
   Holdings  
 Anti-TNFalpha MAb -- Genzyme  
 Anti-TNFalpha MAb B-C7 -- Diaclone  
 Anti-tooth decay MAb -- Planet BioTech.  
 Anti-TRAIL receptor-1 MAb -- Takeda  
 Antitumour RNases -- NIH  
 Anti-VCAM MAb 2A2 -- Alexion  
 Anti-VCAM MAb 3F4 -- Alexion  
 Anti-VCAM-1 MAb  
 Anti-VEC MAb -- ImClone  
 Anti-VEGF MAb -- Genentech  
 Anti-VEGF MAb 2C3  
 Anti-VEGF sheep MAb -- KS Biomedix  
   Holdings  
 Anti-VLA-4 MAb HP1/2 -- Biogen  
 Anti-VLA-4 MAb PS/2  
 Anti-VLA-4 MAb R1-2  
 Anti-VLA-4 MAb TA-2  
 Anti-VAP-1 human MAb  
 Anti-VRE sheep MAb -- KS Biomedix  
   Holdings  
 ANUP -- TranXenoGen  
 ANUP-1 -- Pharis

AOP-RANTES -- Senetek  
 Apan-CH -- Praecis Pharmaceuticals  
 APC-8024 -- Demegen  
 ApoA-1 -- Milano, Pharmacia  
 Apogen -- Alexion  
 apolipoprotein A1 -- Avanir  
 Apolipoprotein E -- Bio-Tech. General  
 Applaggin -- Biogen  
 aprotinin -- ProdiGene  
 APT-070C -- AdProTech  
 AR 177 -- Aronex Pharmaceuticals  
 AR 209 -- Aronex Pharmaceuticals,  
   Antigenics  
 AR545C  
 ARGENT gene delivery systems -- ARIAD  
 Arresten  
 ART-123 -- Asahi Kasei  
 arylsulfatase B -- BioMarin  
 Arylsulfatase B, Recombinant human --  
   BioMarin  
 AS 1051 -- Ajinomoto  
 ASI-BCL -- Intracell  
 Asparaginase - Merck  
 ATL-101 -- Alizyme  
 Atrial natriuretic peptide -- Pharis  
 Aurintricarboxylic acid-high molecular  
   weight  
 Autoimmune disorders -- GPC  
   Biotech/MorphoSys  
 Autoimmune disorders and transplant  
 rejection -- Bristol-Myers Squibb/Genzyme  
   Tra  
 Autoimmune disorders/cancer --  
   Abgenix/Chiron, CuraGen  
 Autotaxin  
 Avicidin -- NeoRx  
 axogenesis factor-1 -- Boston Life Sciences  
 Axokine -- Regeneron  
 B cell lymphoma vaccine -- Biomira  
 B7-1 gene therapy --  
 BABS proteins -- Chiron

FIG. 28F



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BAM-002 -- Novelos Therapeutics  
 Basiliximab (anti CD25 MAb) -- Novartis  
 Bay-16-9996 -- Bayer  
 Bay-39-9437 -- Bayer  
 Bay-50-4798 -- Bayer  
 BB-10153 -- British Biotech  
 BBT-001 -- Bolder BioTech.  
 BBT-002 -- Bolder BioTech.  
 BBT-003 -- Bolder BioTech.  
 BBT-004 -- Bolder BioTech.  
 BBT-005 -- Bolder BioTech.  
 BBT-006 -- Bolder BioTech.  
 BBT-007 -- Bolder BioTech.  
 BCH-2763 -- Shire  
 BCSF -- Millenium Biologix  
 BDNF -- Regeneron -- Amgen  
 Becapiermin -- Johnson & Johnson, Chiron  
 Bectumomab -- Immunomedics  
 Beriplast -- Aventis  
 Beta-adrenergic receptor gene therapy --  
 University of Arkansas  
 bFGF -- Scios  
 BI 51013 -- Behringwerke AG  
 BIBH 1 -- Boehringer Ingelheim  
 BIM-23190 -- Beaufour-Ipsen  
 birch pollen immunotherapy -- Pharmacia  
 bispecific fusion proteins -- NIH  
 Bispecific MAb 2B1 -- Chiron  
 Bitistatin  
 BIWA 4 -- Boehringer Ingelheim  
 blood substitute -- Northfield, Baxter Intl.  
 BLP-25 -- Biomira  
 BLS-0597 -- Boston Life Sciences  
 BLyS -- Human Genome Sciences  
 BLyS radiolabelled -- Human Genome  
 Sciences  
 BM 06021 -- Boehringer Mannheim  
 BM-202 -- BioMarin  
 BM-301 -- BioMarin  
 BM-301 -- BioMarin  
 BM-302 -- BioMarin  
 BMP 2 -- Genetics Institute/Medtronic-  
 Sofamor Danek, Genetics Institute/  
 Collagenesis, Genetics  
 Institute/Yamanouch  
 BMP 2 gene therapy  
 BMP 52 -- Aventis Pasteur, Biopharm  
 BMP-2 -- Genetics Institute  
 BMS 182248 -- Bristol-Myers Squibb  
 BMS 202448 -- Bristol-Myers Squibb  
 bone growth factors -- IsoTis  
 BPC-15 -- Pfizer  
 brain natriuretic peptide --  
 Breast cancer -- Oxford  
 GlycoSciences/Medarex  
 Breast cancer vaccine -- Therion Biologics,  
 Oregon  
 BSSL -- PPL Therapeutics  
 BST-2001 -- BioStratum  
 BST-3002 -- BioStratum  
 BTI 322 --  
 butyrylcholinesterase -- Shire  
 C 6822 -- COR Therapeutics  
 C1 esterase inhibitor -- Pharming  
 C3d adjuvant -- AdProTech  
 CAB-2.1 -- Millennium  
 calcitonin -- Inhale Therapeutics Systems,  
 Aventis, Genetronics, TranXenoGen,  
 Unigene, Rhone Poulenc Rohrer  
 calcitonin -- oral -- Nobex, Emisphere,  
 Pharmaceutical Discovery  
 Calcitonin gene-related peptide -- Asahi  
 Kasei -- Unigene  
 calcitonin, human -- Suntory  
 calcitonin, nasal -- Novartis, Unigene  
 calcitonin, Panoderm -- Elan  
 calcitonin, Peptitrol -- Shire  
 calcitonin, salmon -- Therapicon  
 calin -- Biopharm  
 Calphobindin I  
 calphobindin I -- Kowa  
 calreticulin -- NYU

FIG. 28G

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Campath-1G  
 Campath-1M  
 cancer therapy -- Cangene  
 cancer vaccine -- Aixlie, Aventis Pasteur,  
 Center of Molecular Immunology, YM  
 BioSciences, Cytos, Genzyme,  
 Transgenics, GlobelImmune, Igeneon,  
 ImClone, Virogenetics, InterCell, Iomai,  
 Jenner Biotherapies, Memorial Sloan-  
 Kettering Cancer Center, Sydney Kimmel  
 Cancer Center, Novavax, Protein  
 Sciences, Argonex, SIGA  
 Cancer vaccine ALVAC-CEA B7.1 --  
 Aventis Pasteur/Therion Biologics  
 Cancer vaccine CEA-TRICOM -- Aventis  
 Pasteur/Therion Biologics  
 Cancer vaccine gene therapy -- Cantab  
 Pharmaceuticals  
 Cancer vaccine HER-2/neu -- Corixa  
 Cancer vaccine THERATOPE -- Biomira  
 cancer vaccine, PolyMASC -- Valentis  
 Candida vaccine -- Corixa, Inhibitex  
 Canstatin -- ILEX  
 CAP-18 -- Panorama  
 Cardiovascular gene therapy -- Collateral  
 Therapeutics  
 carperitide -- Suntory  
 Casocidin-1 -- Pharis  
 CAT 152 -- Cambridge Antibody Tech.  
 CAT 192 -- Cambridge Antibody Tech.  
 CAT 213 -- Cambridge Antibody Tech.  
 Catalase-- Enzon  
 Cat-PAD -- Circassia  
 CB 0006 -- Celltech  
 CCK(27-32)-- Akzo Nobel  
 CCR2-64I -- NIH  
 CD, Procept -- Paligent  
 CD154 gene therapy  
 CD39 -- Immunex  
 CD39-L2 -- Hyseq  
 CD39-L4 -- Hyseq  
 CD4 fusion toxin -- Senetek  
 CD4 IgG -- Genentech  
 CD4 receptor antagonists --  
 Pharmacocepeia/Progenics  
 CD4 soluble -- Progenics  
 CD4, soluble -- Genzyme Transgenics  
 CD40 ligand -- Immunex  
 CD4-ricin chain A -- Genentech  
 CD59 gene therapy -- Alexion  
 CD8 TIL cell therapy -- Aventis Pasteur  
 CD8, soluble -- Avidex  
 CD95 ligand -- Roche  
 CDP 571 -- Celltech  
 CDP 850 -- Celltech  
 CDP-860 (PEG-PDGF MAb) -- Celltech  
 CDP 870 -- Celltech  
 CDS-1 -- Ernest Orlando  
 Cedelizumab -- Ortho-McNeil  
 Cetermin -- Insmad  
 CETP vaccine -- Avant  
 Cetorelix  
 Cetuximab  
 CGH 400 -- Novartis  
 CGP 42934 -- Novartis  
 CGP 51901 -- Tanox  
 CGRP -- Unigene  
 CGS 27913 -- Novartis  
 CGS 32359 -- Novartis  
 Chagas disease vaccine -- Corixa  
 chemokines -- Immune Response  
 CHH 380 -- Novartis  
 chitinase -- Genzyme, ICOS  
 Chlamydia pneumoniae vaccine -- Antex  
 Biologics  
 Chlamydia trachomatis vaccine -- Antex  
 Biologics  
 Chlamydia vaccine -- GlaxoSmithKline  
 Cholera vaccine CVD 103-HgR -- Swiss  
 Serum and Vaccine Institute Berne  
 Cholera vaccine CVD 112 -- Swiss Serum  
 and Vaccine Institute Berne

FIG. 28H

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Cholera vaccine inactivated oral -- SBL Vaccin	CRL 1605 -- CytRx
Chrysalin -- Chrysalis BioTech.	CS-560 -- Sankyo
CI-782 -- Hitachi Kase	CSF -- ZymoGenetics
Ciliary neurotrophic factor -- Fidia, Roche	CSF-G -- Hangzhou, Dong-A, Hanmi
CIM project -- Active Biotech	CSF-GM -- Cangene, Hunan, LG Chem
CL 329753 -- Wyeth-Ayerst	CSF-M -- Zarix
CL22, Cobra -- ML Laboratories	CT 1579 -- Merck Frosst
Clenoliximab -- IDEC	CT 1786 -- Merck Frosst
Clostridium difficile antibodies -- Epicyte	CT-112 <sup>A</sup> -- BTG
clotting factors -- Octagene	CTB-134L -- Xenova
CMB 401 -- Celltech	CTC-111 -- Kaketsuken
CNTF -- Sigma-Tau	CTGF -- FibroGen
Cocaine abuse vaccine -- Cantab, ImmuLogic, Scripps	CTLA4-Ig -- Bristol-Myers Squibb
coccidiomycosis vaccine -- Arizo	CTLA4-Ig gene therapy --
collagen -- Type I -- Pharming	CTP-37 -- AVI BioPharma
Collagen formation inhibitors -- FibroGen	C-type natriuretic peptide -- Suntory
Collagen/hydroxyapatite/bone growth factor -- Aventis Pasteur, Biopharm, Orquest	CVS 995 -- Corvas Intl.
collagenase -- BioSpecifics	CX 397 -- Nikko Kyodo
Colorectal cancer vaccine -- Wistar Institute	CY 1747 -- Epimmune
Component B, Recombinant -- Sero	CY 1748 -- Epimmune
Connective tissue growth factor inhibitors -- FibroGen/Taisho	Cyanovirin-N
Contortrostatin	Cystic fibrosis therapy -- CBR/IVAX
contraceptive vaccine -- Zonagen	CYT 351
Contraceptive vaccine hCG	cytokine Traps -- Regeneron
Contraceptive vaccine male reversible -- IMMUCON	cytokines -- Enzon, Cytodonal
Contraceptive vaccine zona pellucida -- Zonagen	Cytomegalovirus glycoprotein vaccine -- Chiron, Aquila Biopharmaceuticals, Aventis Pasteur, Virogenetics
Copper-64 labelled Mab TETA-1A3 -- NCI	Cytomegalovirus vaccine live -- Aventis Pasteur
Coralyne	Cytosine deaminase gene therapy -- GlaxoSmithKline
Corsevin M	DA-3003 -- Dong-A
C-peptide analogues -- Schwarz	DAB389interleukin-6 -- Senetek
CPI-1500 -- Consensus	DAB389interleukin-7
CRF -- Neurobiological Tech.	DAC:GLP-2 -- ConjuChem, Inc.
cRGDfV pentapeptide --	Daclizumab (anti-IL2R Mab) -- Protein Design Labs
CRL 1095 -- CytRx	DAMP <sup>A</sup> -- Incyte Genomics
CRL 1336 -- CytRx	Daniplestim -- Pharmacia
	darbepoetin alfa -- Amgen

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DBI-3019 -- Diabetogen  
 DCC -- Genzyme  
 DDF -- Hyseq  
 decorin -- Integra, Telios  
 defensins -- Large Scale Biology  
 DEGR-VIIa  
 Delmmunised antibody 3B6/22 AGEN  
 Deimmunised anti-cancer antibodies --  
     Biovation/Viragen  
 Dendroamide A  
 Dengue vaccine -- Bavarian Nordic, Merck  
 denileukin diftotox -- Ligand  
 DES-1101 -- Desmos  
 desirudin -- Novartis  
 desmopressin -- Unigene  
 Desmotepase -- Merck, Schering AG  
 Destablase  
 Diabetes gene therapy -- DeveloGen, Pfizer  
 Diabetes therapy -- Crucell  
 Diabetes type 1 vaccine -- Diamyd  
     Therapeutics  
 DiaCIM -- YM BioSciences  
 dialytic oligopeptides -- Research Corp  
 Diamyd -- Diamyd Therapeutics  
 DiaPep227 -- Pepgen  
 DiavaX -- Corixa  
 Digoxin MAb -- Glaxo  
 Diphtheria tetanus pertussis-hepatitis B  
     vaccine -- GlaxoSmithKline  
 DIR therapy -- Solis Therapeutics --  
 DNase -- Genentech  
 Dornase alfa -- Genentech  
 Dornase alfa, inhalation -- Genentech  
 Doxorubicin-anti-CEA MAb conjugate --  
     Immunomedics  
 DP-107 -- Trimeris  
 drotrecogin alfa -- Eli Lilly  
 DTctGMCSF  
 DTP-polio vaccine -- Aventis Pasteur  
 DU 257-KM231 antibody conjugate --  
     Kyowa  
     dural graft matrix -- Integra  
     Duteplase -- Baxter Intl.  
     DWP-401 -- Daewoong  
     DWP-404 -- Daewoong  
     DWP-408 -- Daewoong  
     Dx 88 (Epi-KAL2) -- Dyax  
     Dx 890 (elastin inhibitors) -- Dyax  
     E coli O157 vaccine -- NIH  
     E21-R -- BresaGen  
     Eastern equine encephalitis virus vaccine --  
     Echicetin --  
     Echinhibin 1 --  
     Echistatin -- Merck  
     Echitamine --  
     Ecromeximab -- Kyowa Hakko  
     EC-SOD -- PPL Therapeutics  
     Eculizumab (5G1.1) -- Alexion  
     EDF -- Ajinomoto  
     EDN derivative -- NIH  
     EDNA -- NIH  
     Edobacomab -- XOMA  
     Edrecolomab -- Centocor  
     EF 5077  
     Efalizumab -- Genentech  
     EGF fusion toxin -- Seragen, Ligand  
     EGF-P64k vaccine -- Center of Molecular  
         Immunology  
     EL 246 -- LigoCyte  
     elastase inhibitor -- Synergen  
     elcatonin -- Therapicon  
     EMD 72000 -- Merck KGaA  
     Emdogain -- BIORA  
     emfilermin -- AMRAD  
     Emoctakin -- Novartis  
     enamel matrix protein -- BIORA  
     Endo III -- NYU  
     endostatin -- EntreMed, Pharis  
     Enhancins -- Micrologix  
     Enlimomab -- Isis Pharm.  
     Enoxaparin sodium -- Phamuka

FIG. 28J

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enzyme linked antibody nutrient depletion  
 therapy -- KS Biomedix Holdings  
 Eosinophil-derived neutralizing agent --  
 EP-51216 -- Asta Medica  
 EP-51389 -- Asta Medica  
 EPH family ligands -- Regeneron  
 Epidermal growth factor -- Hitachi Kasei,  
 Johnson & Johnson  
 Epidermal growth factor fusion toxin --  
 Senetek  
 Epidermal growth factor-genistein --  
 EPI-HNE-4 -- Dyax  
 EPI-KAL2 -- Dyax  
 Epoetin-alfa -- Amgen, Dragon  
 Pharmaceuticals, Nanjing Huaxin  
 Epratuzumab -- Immunomedics  
 Epstein-Barr virus vaccine --  
 Aviron/SmithKline Beecham, Bioresearch  
 Eptacog alfa -- Novo Nordisk  
 Eptifibatide -- COR Therapeutics  
 erb-38 --  
 Erlizumab -- Genentech  
 erythropoietin -- Alkermes, ProLease, Dong-  
 A, Elanex, Genetics Institute, LG Chem,  
 Protein Sciences, Serono, Snow Brand,  
 SRC VB VECTOR, Transkaryotic  
 Therapies  
 Erythropoietin Beta -- Hoffman La Roche  
 Erythropoietin/Epoetin alfa -- Chugai  
 Escherichia coli vaccine -- North American  
 Vaccine, SBL Vaccin, Swiss Serum and  
 Vaccine Institute Berne  
 etanercept -- Immunex  
 examorelin -- Mediolanum  
 Exendin 4 -- Amylin  
 exonuclease VII  
 F 105 -- Centocor  
 F-992 -- Fornix  
 Factor IX -- Alpha Therapeutics, Welfide  
 Corp., CSL, enetics Institute/AHP,  
 Pharmacia, PPL Therapeutics  
 Factor IX gene therapy -- Cell Genesys  
 Factor VII -- Novo Nordisk, Bayer, Baxter  
 Intl.  
 Factor VIIa -- PPL Therapeutics,  
 ZymoGenetics  
 Factor VIII -- Bayer Genentech, Beaufour-  
 Ipsen, CLB, Inex, Octagen, Pharmacia,  
 Pharming  
 Factor VIII -- PEGylated -- Bayer  
 Factor VIII fragments -- Pharmacia  
 Factor VIII gene therapy -- Targeted  
 Genetics  
 Factor VIII sucrose formulation -- Bayer,  
 Genentech  
 Factor VIII-2 -- Bayer  
 Factor VIII-3 -- Bayer  
 Factor Xa inhibitors -- Merck, Novo Nordisk,  
 Mochida  
 Factor XIII -- ZymoGenetics  
 Factors VIII and IX gene therapy -- Genetics  
 Institute/Targeted Genetics  
 Famoxin -- Genset  
 Fas (delta) TM protein -- LXR BioTech.  
 Fas TR -- Human Genome Sciences  
 Felvizumab -- Scotgen  
 FFR-VIIa -- Novo Nordisk  
 FG-001 -- F-Gene  
 FG-002 -- F-Gene  
 FG-004 -- F-Gene  
 FG-005 -- F-Gene  
 FGF + fibrin -- Repair  
 Fibrimage -- Bio-Tech. General  
 fibrin-binding peptides -- ISIS Innovation  
 fibrinogen -- PPL Therapeutics, Pharming  
 fibroblast growth factor -- Chiron, NYU,  
 Ramot, ZymoGenetics  
 fibrolase conjugate -- Schering AG  
 Filgrastim -- Amgen  
 filgrastim -- PDA modified -- Xencor  
 FLT-3 ligand -- Immunex  
 FN18 CRM9 --

FIG. 28K

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follistatin -- Biotech Australia, Human Therapeutics  
 follitropin alfa -- Alkermes, ProLease, PowderJect, Serono, Akzo Nobel  
 Follitropin Beta -- Bayer, Organon  
 FP 59  
 FSH -- Ferring  
 FSH + LH -- Ferring  
 F-spondin -- CeNeS  
 fusion protein delivery system -- UAB Research Foundation  
 fusion toxins -- Boston Life Sciences  
 G 5598 -- Genentech  
 GA-II -- Transkaryotic Therapies  
 Gamma-interferon analogues -- SRC VB VECTOR  
 Ganirelix -- Roche  
 gastric lipase -- Meristem  
 Gavilimomab --  
 G-CSF -- Amgen, SRC VB VECTOR  
 GDF-1 -- CeNeS  
 GDF-5 -- Biopharm  
 GDNF (glial derived neurotrophic factor) -- Amgen  
 gelsolin -- Biogen  
 Gemtuzumab ozogamicin -- Celltech  
 Gene-activated epoetin-alfa -- Aventis Pharma -- Transkaryotic Therapies  
 Glanzmann thrombasthenia gene therapy --  
 Glatiramer acetate -- Yeda  
 glial growth factor 2 -- CeNeS  
 GLP-1 -- Amylin, Suntory, TheraTech, Watson  
 GLP-1 peptide analogues -- Zealand Pharmaceuticals  
 GLP-2 -- Novo Nordisk, Ontario, Inc., Suntory Limited  
 glucagon -- Eli Lilly, ZymoGenetics  
 Glucagon-like peptide 1-7-36 amide -- Suntory  
 Glucogen-like peptide -- Amylin  
 Glucocerebrosidase -- Genzyme  
 glutamate decarboxylase -- Genzyme Transgenics  
 Glycoprotein S3 -- Kureha  
 GM-CSF -- Immuhex  
 GM-CSF tumour vaccine -- PowderJect  
 GnRH immunotherapeutic -- Protherics  
 Goserelin (LhRH antagonist) -- AstraZeneca  
 gp75 antigen -- ImClone  
 gp96 -- Antigenics  
 GPI 0100 -- Galenica  
 GR 4991W93 -- GlaxoSmithKline  
 Granulocyte colony-stimulating factor -- Dong-A  
 Granulocyte colony-stimulating factor conjugate  
 grass allergy therapy -- Dynavax  
 GRF1-44 -- ICN  
 Growth Factor -- Chiron, Atrigel, Atrix, Innogenetics, ZymoGenetics, Novo  
 growth factor peptides -- Biotherapeutics  
 growth hormone -- LG Chem  
 growth hormone, Recombinant human -- Serono  
 GT 4086 -- Gliatech  
 GW 353430 -- GlaxoSmithKline  
 GW-278884 -- GlaxoSmithKline  
 H 11 -- Viventia Biotech  
 H5N1 influenza A virus vaccine -- Protein Sciences  
 haemoglobin -- Biopure  
 haemoglobin 3011, Recombinant -- Baxter Healthcare  
 haemoglobin crosumaril -- Baxter Intl.  
 haemoglobin stabilized -- Ajinomoto  
 haemoglobin, recombinant -- Apex  
 HAF -- Immune Response  
 Hantavirus vaccine  
 HB 19  
 HBNF -- Regeneron  
 HCC-1 -- Pharis

FIG. 28L

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hCG -- Milkhaus  
 hCG vaccine -- Zonagen  
 HE-317 -- Hollis-Eden Pharmaceuticals  
 Heat shock protein cancer and influenza  
 vaccines -- StressGen  
 Helicobacter pylori vaccine -- Acambis,  
 AstraZeneca/CSL, Chiron, Provalis  
 Helistat-G -- GalaGen  
 Hemolink -- Hemosol  
 hepapoietin -- Snow Brand  
 heparanase -- InSight  
 heparinase I -- Ibex  
 heparinase III -- Ibex  
 Hepatitis A vaccine -- American Biogenetic  
 Sciences  
 Hepatitis A vaccine inactivated  
 Hepatitis A vaccine Nothav -- Chiron  
 Hepatitis A-hepatitis B vaccine --  
 GlaxoSmithKline  
 hepatitis B therapy -- Tripep  
 Hepatitis B vaccine -- Amgen, Chiron SpA,  
 Meiji Milk, NIS, Prodeva, PowderJect,  
 Rhein Biotech  
 Hepatitis B vaccine recombinant -- Evans  
 Vaccines, Epitex Combiotech, Genentech,  
 MedImmune, Merck Sharp & Dohme,  
 Rhein Biotech, Shantha Biotechnics,  
 Vector, Yeda  
 Hepatitis B vaccine recombinant TGP 943 --  
 Takeda  
 Hepatitis C vaccine -- Bavarian Nordic,  
 Chiron, Innogenetics Acambis,  
 Hepatitis D vaccine -- Chiron Vaccines  
 Hepatitis E vaccine recombinant --  
 Genelabs/GlaxoSmithKline, Novavax  
 hepatocyte growth factor -- Panorama,  
 Sosei  
 hepatocyte growth factor kringle fragments -  
 - Entremed  
 Her-2/Neu peptides -- Corixa  
 Herpes simplex glycoprotein DNA vaccine --  
 Merck, Wyeth-Lederle Vaccines-Malvern,  
 Genentech, GlaxoSmithKline, Chiron,  
 Takeda  
 Herpes simplex vaccine -- Cantab  
 Pharmaceuticals, CEL-SCI, Henderson  
 Morley  
 Herpes simplex vaccine live -- ImClone  
 Systems/Wyeth-Lederle, Aventis Pasteur  
 HGF derivatives -- Dompe  
 hAPP vaccine -- Crucell  
 Hib-hepatitis B vaccine -- Aventis Pasteur  
 HIC 1  
 HIP-- Altachem  
 Hirudins -- Biopharma, Cangene, Dongkook,  
 Japan Energy Corporation, Pharmacia  
 Corporation, SIR International, Sanofi-  
 Synthelabo, Sotragene, Rhein Biotech  
 HIV edible vaccine -- ProdiGene  
 HIV gp120 vaccine -- Chiron, Ajinomoto,  
 GlaxoSmithKline, ID Vaccine, Progenics,  
 VaxGen  
 HIV gp120 vaccine gene therapy --  
 HIV gp160 DNA vaccine -- PowderJect,  
 Aventis Pasteur, Oncogen, Hyland  
 Immuno, Protein Sciences  
 HIV gp41 vaccine -- Panacos  
 HIV HGP-30W vaccine -- CEL-SCI  
 HIV immune globulin -- Abbott, Chiron  
 HIV peptides -- American Home Products  
 HIV vaccine -- Applied bioTech., Axis  
 Genetics, Biogen, Bristol-Myers Squibb,  
 Genentech, Korea Green Cross, NIS,  
 Oncogen, Protein Sciences Corporation,  
 Terumo, Tonen Corporation, Wyeth-  
 Ayerst, Wyeth-Lederle Vaccines-Malvern,  
 Advanced BioScience Laboratories,  
 Bavarian Nordic, Bavarian Nordic/Statens  
 Serum Institute, GeneCure, Immune  
 Response, Progenics, Theron Biologics,  
 United Biomedical, Chiron

FIG. 28M

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HIV vaccine vCP1433 -- Aventis Pasteur  
 HIV vaccine vCP1452 -- Aventis Pasteur  
 HIV vaccine vCP205 -- Aventis Pasteur  
 HL-9 -- American BioScience  
 HM-9239 -- Cytran  
 HML-103 -- Hemosol  
 HML-104 -- Hemosol  
 HML-105 -- Hemosol  
 HML-109 -- Hemosol  
 HML-110 -- Hemosol  
 HML-121 -- Hemosol  
 hNLP -- Pharis  
 Hookworm vaccine  
 host-vector vaccines -- Henogen  
 HPM 1 -- Chugai  
 HPV vaccine -- MediGene  
 HSA -- Meristem  
 HSF -- StressGen  
 HSP carriers -- Weizmann, Yeda, Peptor  
 HSPPC-70 -- Antigenics  
 HSPPC-96, pathogen-derived -- Antigenics  
 HSV 863 -- Novartis  
 HTLV-I DNA vaccine  
 HTLV-I vaccine  
 HTLV-II vaccine -- Access  
 HU 901 -- Tanox  
 Hu23F2G -- ICOS  
 HuHMF1  
 HumaLYM -- Intracell  
 Human krebs statika -- Yamanouchi  
 human monoclonal antibodies --  
   Abgenix/Biogen, Abgenix/ Corixa,  
   Abgenix/immunex, Abgenix/Lexicon,  
   Abgenix/ Pfizer, Athersys/Medarex,  
   Biogen/MorphoSys, CAT/Searle,  
   Centocor/Medarex, Corixa/Kirin Brewery,  
   Corixa/Medarex, Eos BioTech./Medarex,  
   Eos/Xenex, Exelixis/Protein Design  
   Labs, ImmunoGen/ Raven, Medarex/  
   B.Twelve, MorphoSys/ImmunoGen, XTL  
   Biopharmaceuticals/Dyax,  
 Human monoclonal antibodies --  
   Medarex/Northwest Biotherapeutics,  
   Medarex/Seattle Genetics  
 human netrin-1 -- Exelixis  
 human papillomavirus antibodies -- Epicyte  
 Human papillomavirus vaccine -- Biotech  
   Australia, IDEC, StressGen  
 Human papillomavirus vaccine MEDI 501 --  
   MedImmune/GlaxoSmithKline  
 Human papillomavirus vaccine MEDI  
   503/MEDI 504 --  
   MedImmune/GlaxoSmithKline  
 Human papillomavirus vaccine TA-CIN --  
   Cantab Pharmaceuticals  
 Human papillomavirus vaccine TA-HPV --  
   Cantab Pharmaceuticals  
 Human papillomavirus vaccine TH-GW --  
   Cantab/GlaxoSmithKline  
 human polyclonal antibodies -- Biosite/Eos  
   BioTech./ Medarex  
 human type II anti factor VIII monoclonal  
   antibodies -- ThromboGenics  
 humanised anti glycoprotein Ib murine  
   monoclonal antibodies -- ThromboGenics  
 HumaRAD -- Intracell  
 HuMax EGFR -- Genmab  
 HuMax-CD4 -- Medarex  
 HuMax-IL15 -- Genmab  
 HYB 190 -- Hybridon  
 HYB 676 -- Hybridon  
 I-125 Mab A33 -- Celltech  
 Ibritumomab tiuxetan -- IDEC  
 IBT-9401 -- Ibx  
 IBT-9402 -- Ibx  
 IC 14 -- ICOS  
 Idarubicin anti-Ly-2.1 --  
 IDEC 114 -- IDEC  
 IDEC 131 -- IDEC  
 IDEC 152 -- IDEC  
 IDM 1 -- IDM  
 IDPS -- Hollis-Eden Pharmaceuticals

FIG. 28N



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iduronate-2-sulfatase -- Transkaryotic Therapies  
 IGF/IBP-2-13 -- Pharis  
 IGN-101 -- Igeneon  
 IK HIR02 -- Iketon  
 IL-11 -- Genetics Institute/AHP  
 IL-13-PE38 -- NeoPharm  
 IL-17 receptor -- Immunex  
 IL-18BP -- Yeda  
 IL-1Hy1 -- Hyseq  
 IL-1 $\beta$  -- Celltech  
 IL-1 $\beta$  adjuvant -- Celltech  
 IL-2 -- Chiron  
 IL-2 + IL-12 -- Hoffman La-Roche  
 IL-6/sIL-6R fusion -- Hadasit  
 IL-6R derivative -- Tosoh  
 IL-7-Dap 389 fusion toxin -- Ligand  
 IL-21 -- Novo Nordisk, ZymoGenetics  
 IM-862 -- Cytran  
 IMC-1C11 -- ImClone  
 imiglucerase -- Genzyme  
 Immune globulin intravenous (human) -- Hoffman La Roche  
 immune privilege factor -- Proneuron  
 Immunocal -- Immunotec  
 Immunogene therapy -- Briana Bio-Tech  
 Immunoliposomal 5-fluorodeoxyuridine-dipalmitate --  
 immunosuppressant vaccine -- Aixlie  
 immunotoxin -- Antisoma, NIH  
 ImmuRAIT-Re-188 -- Immunomedics  
 imreg-1 -- Imreg  
 infertility -- Johnson & Johnson, E-TRANS  
 Infliximab -- Centocor  
 Influenza virus vaccine -- Aventis Pasteur, Protein Sciences  
 inhibin -- Biotech Australia, Human Therapeutics  
 Inhibitory G protein gene therapy  
 INKP-2001 -- InKine  
 Inolimomab -- Diaclone  
 insulin -- AutoImmune, Altea, Biobras, BioSante, Bio-Tech. General, Chong Kun Dang, Emisphere, Flamel, Provalis, Rhein Biotech, TranXenoGen  
 insulin (bovine) -- Novartis  
 insulin analogue -- Eli Lilly  
 Insulin Aspart -- Novo Nordisk  
 insulin detemir -- Novo Nordisk  
 insulin glargine -- Aventis  
 insulin inhaled -- Inhale Therapeutics Systems, Alkermes  
 insulin oral -- Inovax  
 insulin, AeroDose -- AeroGen  
 insulin, AERx -- Aradigm  
 insulin, BEODAS -- Elan  
 insulin, Biphasix -- Helix  
 insulin, buccal -- Generex  
 insulin, I2R -- Flemington  
 insulin, intranasal -- Bentley  
 insulin, oral -- Nobex, Unigene  
 insulin, Orasome -- Endorex  
 insulin, ProMaxx -- Epic  
 insulin, Quadrant -- Elan  
 insulin, recombinant -- Aventis  
 insulin, Spiros -- Elan  
 insulin, Transfersome -- IDEA  
 insulin, Zymo, recombinant -- Novo Nordisk  
 insulinotropin -- Scios  
 Insulysin gene therapy --  
 integrin antagonists -- Merck  
 interferon (Alpha2) -- SRC VB VECTOR, Viragen, Dong-A, Hoffman La-Roche, Genentech  
 interferon -- BioMedicines, Human Genome Sciences  
 interferon (Alfa-n3) -- Interferon Sciences Intl.  
 interferon (Alpha), Biphasix -- Helix

FIG. 280

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interferon (Alpha)—Amgen, BioNative,  
 Novartis, Genzyme Transgenics,  
 Hayashibara, Inhale Therapeutics  
 Systems, Medusa, Flamel, Dong-A,  
 GeneTrol, Nasteck, Shantha,  
 Wassermann, LG Chem, Sumitomo,  
 Aventis, Behring EGIS, Pepgen, Servier,  
 Rhein Biotech,  
 interferon (Alpha2A)  
 interferon (Alpha2B) — Enzon, Schering-  
 Plough, Biogen, IDEA  
 interferon (Alpha-N1) — GlaxoSmithKline  
 interferon (beta) — Rentschler, GeneTrol,  
 Meristem, Rhein Biotech, Toray, Yeda,  
 Daiichi, Mochida  
 interferon (Beta1A) — Sero, Biogen  
 interferon (beta1A), inhale — Biogen  
 interferon (β1b)— Chiron  
 interferon (tau)— Pepgen  
 Interferon alfacon-1 — Amgen  
 Interferon alpha-2a vaccine  
 Interferon Beta 1b — Schering/Chiron,  
 InterMune  
 Interferon Gamma — Boehringer Ingelheim,  
 Sheffield, Rentschler, Hayashibara  
 interferon receptor, Type I — Sero  
 interferon (Gamma1B) — Genentech  
 Interferon-alpha-2b + ribavirin — Biogen,  
 ICN  
 Interferon-alpha-2b gene therapy —  
 Schering-Plough  
 Interferon-con1 gene therapy —  
 interleukin-1 antagonists — Dompe  
 Interleukin-1 receptor antagonist — Abbott  
 Bioresearch, Pharmacia  
 Interleukin-1 receptor type I — Immunex  
 interleukin-1 receptor Type II — Immunex  
 Interleukin-1 trap — Regeneron  
 Interleukin-1-alpha — Immunex/Roche  
 interleukin-2 — SRC VB VECTOR,  
 Ajinomoto, Biomira, Chiron  
 IL-2/ diphtheria toxin — Ligand  
 Interleukin-3 — Cangene  
 Interleukin-4 — Immunology Ventures,  
 Sanofi Winthrop, Schering-Plough,  
 Immunex/ Sanofi Winthrop, Bayer, Ono  
 interleukin-4 + TNF-Alpha — NIH  
 interleukin-4 agonist — Bayer  
 interleukin-4 fusion toxin — Ligand  
 Interleukin-4 receptor — Immunex, Immun  
 Interleukin-6 — Ajinomoto, Cangene, Yeda,  
 Genetics Institute, Novartis  
 interleukin-6 fusion protein  
 interleukin-6 fusion toxin — Ligand, Sero  
 interleukin-7 — IC Innovations  
 interleukin-7 receptor — Immunex  
 interleukin-8 antagonists — Kyowa  
 Hakko/Millennium/Pfizer  
 interleukin-9 antagonists — Genaera  
 Interleukin-10 — DNAX, Schering-Plough  
 Interleukin-10 gene therapy —  
 interleukin-12 — Genetics Institute, Hoffman  
 La-Roche  
 interleukin-13 — Sanofi  
 interleukin-13 antagonists — AMRAD  
 Interleukin-13-PE38QQR  
 interleukin-15 — Immunex  
 interleukin-16 — Research Corp  
 Interleukin-18 — GlaxoSmithKline  
 Interleukin-18 binding protein — Sero  
 Ior-P3 — Center of Molecular Immunology  
 IP-10 — NIH  
 IPF — Metabolex  
 IR-501 — Immune Response  
 ISIS 9125 — Isis Pharmaceuticals  
 ISURF No. 1554 — Millennium  
 ISURF No. 1866 — Iowa State Univer.  
 ITF-1697 — Italfarmaco  
 IxC 162 — Ixion  
 J 695 — Cambridge Antibody Tech.,  
 Genetics Inst., Knoll  
 Jagged + FGF — Repair

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JKC-362 -- Phoenix Pharmaceuticals  
 JTP-2942 -- Japan Tobacco  
 Juman monoclonal antibodies --  
     Medarex/Raven  
 K02 -- Axyx Pharmaceuticals  
 Keliximab -- IDEC  
 Keyhole limpet haemocyanin  
 KGF -- Amgen  
 KM 871 -- Kyowa  
 KPI 135 -- Scios  
 KPI-022 -- Scios  
 Kringle 5  
 KSB 304  
 KSB-201 -- KS Biomedex  
 L 696418 -- Merck  
 L 703801 -- Merck  
 L1 -- Acorda  
 L-761191 -- Merck  
 lactoferrin -- Meristem, Pharming, Agennix  
 lactoferrin cardio -- Pharming  
 LAG-3 -- Seroxo  
 LAIT -- GEMMA  
 LAK cell cytotoxin -- Arizona  
 lamellarins -- PharmaMar/University of  
     Malaga  
 laminin A peptides -- NIH  
 lanoteplase -- Genetics Institute  
 laronidase -- BioMarin  
 Lassa fever vaccine  
 LCAT -- NIH  
 LDP 01 -- Millennium  
 LDP 02 -- Millennium  
 Lecithinized superoxide dismutase --  
     Seikagaku  
 LeIF adjuvant -- Corixa  
 leishmaniasis vaccine -- Corixa  
 lenercept -- Hoffman La-Roche  
 Lenograstim -- Aventis, Chugai  
 lepirudin -- Aventis  
 leptin -- Amgen, IC Innovations  
 Leptin gene therapy -- Chiron Corporation  
 leptin, 2nd-generation -- Amgen  
 leridistim -- Pharmacia  
 leuprolide, ProMaxx -- Epic  
 leuprorelin, oral -- Unigene  
 LeuTech -- Papatin  
 LEX 032 -- SuperGen  
 LiDEPT -- Novartis  
 Lintuzumab (anti-CD33 MAb) -- Protein  
     Design Labs  
 lipase -- Altus Biologics  
 lipid A vaccine -- EntreMed  
 lipid-linked anchor Tech. -- ICRT, ID  
     Biomedical  
 liposome-CD4 Tech. -- Sheffield  
 Listeria monocytogenes vaccine  
 LMB 1  
 LMB 7  
 LMB 9 -- Battelle Memorial Institute, NIH  
 LM-CD45 -- Cantab Pharmaceuticals  
 lovastatin -- Merck  
 LSA-3  
 LT- $\beta$  receptor -- Biogen  
 lung cancer vaccine -- Corixa  
 lusupultide -- Scios  
 L-Vax -- AVAX  
 LY 355455 -- Eli Lilly  
 LY 366405 -- Eli Lilly  
 LY-355101 -- Eli Lilly  
 Lyme disease DNA vaccine -- Vical/Aventis  
     Pasteur  
 Lyme disease vaccine -- Aquila  
 Biopharmaceuticals, Aventis, Pasteur,  
 Symbicom, GlaxoSmithKline, Hyland  
 Immuno, MedImmune  
 Lymphocytic choriomeningitis virus vaccine  
 lymphoma vaccine -- Biomira, Genitope  
 LYP18  
 lys plasminogen, recombinant  
 Lysosomal storage disease gene therapy --  
     Avigen  
 lysostaphin -- Nutrition 21

FIG. 28Q

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M 23 -- Gruenenthal  
 M1 monoclonal antibodies -- Acorda  
 Therapeutics  
 MA 16N7C2 -- Corvas Intl.  
 malaria vaccine -- GlaxoSmithKline,  
 AdProTech, Antigenics, Apovia, Aventis  
 Pasteur, Axis Genetics, Behringwerke,  
 CDCP, Chiron Vaccines, Genzyme  
 Transgenics, Hawaii, MedImmune, NIH,  
 NYU, Oxxon, Roche/Saramane, Biotech  
 Australia, Rx Tech  
 Malaria vaccine CDC/NIIMALVAC-1  
 malaria vaccine, multicomponent  
 mammaglobin -- Corixa  
 mammastatin -- Biotherapeutics  
 mannan-binding lectin -- NatlImmu  
 mannan-MUC1 -- Psiron  
 MAP 30  
 Marinovir -- Phytera  
 MARstem -- Maret  
 MB-015 -- Mochida  
 MBP -- ImmuLogic  
 MCI-028 -- Mitsubishi-Tokyo  
 MCIF -- Human Genome Sciences  
 MDC -- Advanced BioScience -- Akzo  
 Nobel, ICOS  
 MDX 11 -- Medarex  
 MDX 210 -- Medarex  
 MDX 22 -- Medarex  
 MDX 22  
 MDX 240 -- Medarex  
 MDX 33  
 MDX 44 -- Medarex  
 MDX 447 -- Medarex  
 MDX H210 -- Medarex  
 MDX RA -- Houston BioTech., Medarex  
 ME-104 -- Pharmexa  
 Measles vaccine  
 Mecasermin -- Cephalon/Chiron, Chiron  
 MEDI 488 -- MedImmune  
 MEDI 500  
 MEDI 507 -- BioTransplant  
 melanin concentrating hormone --  
 Neurocrine Biosciences  
 melanocortins -- OMRF  
 Melanoma monoclonal antibodies -- Viragen  
 melanoma vaccine -- GlaxoSmithKline,  
 Akzo Nobel, Avant, Aventis Pasteur,  
 Bavarian Nordic, Biovector, CancerVax,  
 Genzyme Molecular Oncology, Humbolt,  
 ImClone Systems, Memorial, NYU, Oxxon  
 Melanoma vaccine Magevac -- Therion  
 memory enhancers -- Scios  
 meningococcal B vaccine -- Chiron  
 meningococcal vaccine -- CAMR  
 Meningococcal vaccine group B conjugate -  
 - North American Vaccine  
 Meningococcal vaccine group B  
 recombinant -- BioChem Vaccines,  
 Microscience  
 Meningococcal vaccine group Y conjugate -  
 - North American Vaccine  
 Meningococcal vaccine groups A B and C  
 conjugate -- North American Vaccine  
 Mepolizumab -- GlaxoSmithKline  
 Metastatin -- EntreMed, Takeda  
 Met-CkB7 -- Human Genome Sciences  
 met-enkephalin -- TNI  
 METH-1 -- Human Genome Sciences  
 methioninase -- AntiCancer  
 Methionine lyase gene therapy --  
 AntiCancer  
 Met-RANTES -- Genexa Biomedical,  
 Serono  
 Metreleptin  
 Microtubule inhibitor MAb  
 Immunogen/Abgenix  
 MGDF -- Kirin  
 MGTV -- Progenics  
 micrin -- Endocrine  
 microplasmin -- ThromboGenics  
 MIF -- Genetics Institute

FIG. 28R

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migration inhibitory factor -- NIH	MAb 45-2D9- -- haematoporphyrin conjugate
Mim CD4.1 -- Xycte Therapies	MAb 4B4
mirostipen -- Human Genome Sciences	MAb 4E3-CPA conjugate -- BCM Oncologia
Mitumomab (BEC-2) -- ImClone Systems, Merck KGaA	MAb 4E3-daunorubicin conjugate
MK 852 -- Merck	MAb 50-6
MLN 1202 (Anti-CCR2 monoclonal antibody) -- Millenium Pharmaceuticals	MAb 50-61A -- Institut Pasteur
Mobenakin -- NIS	MAb 5A8 -- Biogen
molgramostim -- Genetics Institute, Novartis	MAb 791T/36-methotrexate conjugate
monoclonal antibodies -- Abgenix/Celltech, Immusol/ Medarex, Viragen/ Roslin Institute, Cambridge Antibody Tech./Elan	MAb 7c11.e8
MAb 108 --	MAb 7E11 C5-selenocystamine conjugate
MAb 10D5 --	MAb 93KA9 -- Novartis
MAb 14.18-interleukin-2 immunocytokine -- Lexigen	MAb A5B7-cisplatin conjugate -- Biodynamics Research, Pharmacia
MAb 14G2a --	MAb A5B7-I-131
MAb 15A10 --	MAb A7
MAb 170 -- Biomira	MAb A717 -- Exocell
MAb 177Lu CC49 --	MAb A7-zinostatin conjugate
MAb 17F9	MAb ABX-RB2 -- Abgenix
MAb 1D7	MAb ACA 11
MAb 1F7 -- Immune Network	MAb AFP-I-131 -- Immunomedics
MAb 1H10-doxorubicin conjugate	MAb AP1
MAb 26-2F	MAb AZ1
MAb 2A11	MAb B3-LysPE40 conjugate
MAb 2E1 -- RW Johnson	MAb B4 -- United Biomedical
MAb 2F5	MAb B43 Genistein-conjugate
MAb 31.1 -- International BioImmune Systems	MAb B43.13-Tc-99m -- Biomira
MAb 32 -- Cambridge Antibody Tech., Peptech	MAb B43-PAP conjugate
MAb 323A3 -- Centocor	MAb B4G7-gelonin conjugate
MAb 3C5	MAb BCM 43-daunorubicin conjugate -- BCM Oncologia
MAb 3F12	MAB BIS-1
MAb 3F8	MAB BMS 181170 -- Bristol-Myers Squibb
MAB 42/6	MAB BR55-2
MAB 425 -- Merck KGaA	MAB BW494
MAB 447-52D -- Merck Sharp & Dohme	MAB C 242-DM1 conjugate -- ImmunoGen
	MAB C242-PE conjugate
	MAB c30-6
	MAB CA208-cytorhodin-S conjugate -- Hoechst Japan
	MAB CC49 -- Enzo

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MAb ch14.18 --	MAb LL2-I-131 -- Immunomedics
MAb CH14.18-GM-CSF fusion protein -- Lexigen	MAb LL2-Y-90
MAb chCE7	MAb LS2D617 -- Hybritech
MAb CI-137 -- AMRAD	MAb LYM-1-gelonin conjugate
MAb cisplatin conjugate	MAb LYM-1-I-131
MAb CLB-CD19	MAb LYM-1-Y-90
MAb CLB-CD19v	MAb LYM-2 -- Peregrine
MAb CLL-1 -- Peregrine	MAb M195
MAb CLL-1-GM-CSF conjugate	MAb M195-bismuth 213 conjugate -- Protein Design Labs
MAb CLL-1-IL-2 conjugate -- Peregrine	MAb M195-gelonin conjugate
MAb CLN IgG -- doxorubicin conjugates	MAb M195-I-131
MAb conjugates -- Tanox	MAb M195-Y-90
MAb D612	MAb MA 33H1 -- Sanofi
MAb Dal B02	MAb MAD11
MAb DC101 -- ImClone	MAb MGb2
MAb EA 1 --	MAb MINT5
MAb EC708 -- Biovation	MAb MK2-23
MAb EP-5C7 -- Protein Design Labs	MAb MOC31 ETA(252-613) conjugate
MAb ERIC-1 -- ICRT	MAb MOC-31-In-111
MAb F105 gene therapy	MAb MOC-31-PE conjugate
MAb FC 2.15	MAb MR6 --
MAb G250 -- Centocor	MAb MRK-16 -- Aventis Pasteur
MAb GA6	MAb MS11G6
MAb GA733	MAb MX-DTPA BrE-3
MAb Gliomab-H -- Viventia Biotech	MAb MY9
MAb HB2-saporin conjugate	MAb Nd2 -- Tosoh
MAb HD 37 --	MAb NG-1 -- Hygeia
MAb HD37-ricin chain-A conjugate	MAb NM01 -- Nissin Food
MAb HNK20 -- Acambis	MAb OC 125
MAb huN901-DM1 conjugate -- ImmunoGen	MAb OC 125-CMA conjugate
MAb I-131 CC49 -- Corixa	MAb OKI-1 -- Ortho-McNeil
MAb ICO25	MAb OX52 -- Bioproducts for Science
MAb ICR12-CPG2 conjugate	MAb PMA5
MAb ICR-62	MAb PR1
MAb IRac-ricin A conjugate	MAb prost 30
MAb K1	MAb R-24
MAb KS1-4-methotrexate conjugate	MAb R-24 $\alpha$ Human GD3 -- Celltech
MAb L6 -- Bristol-Myers Squibb, Oncogen	MAb RFB4-ricin chain A conjugate
MAb LICO 16-88	MAb RFT5-ricin chain A conjugate
	MAb SC 1

FIG. 28T

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MAb SM-3 -- ICRT  
 MAb SMART 1D10 -- Protein Design Labs  
 MAb SMART ABL 364 -- Novartis  
 MAb SN6f  
 MAb SN6f-deglycosylated ricin A chain conjugate --  
 MAb SN6j  
 MAb SN7-ricin chain A conjugate  
 MAb T101-Y-90 conjugate -- Hybritech  
 MAb T-88 -- Chiron  
 MAb TB94 -- Cancer Immunobiology  
 MAb TEC 11  
 MAb TES-23 -- Chugai  
 MAb TM31 -- Avant  
 MAb TNT-1 -- Cambridge Antibody Tech., Peregrine  
 MAb TNT-3  
 MAb TNT-3 -- IL2 fusion protein --  
 MAb TP3-At-211  
 MAb TP3-PAP conjugate --  
 MAb UJ13A -- ICRT  
 MAb UN3  
 MAb ZME-018-gelonin conjugate  
 MAb-BC2 -- GlaxoSmithKline  
 MAb-DM1 conjugate -- ImmunoGen  
 MAb-ricin-chain-A conjugate -- XOMA  
 MAb-temoporfin conjugates  
 Monopharm C -- Viventia Biotech  
 montepelase -- Eisai  
 montirelin hydrate -- Gruenenthal  
 morotocog alfa -- Genetics Institute  
 Morotocog-alfa -- Pharmacia  
 MP 4  
 MP-121 -- Biopharm  
 MP-52 -- Biopharm  
 MRA -- Chugai  
 MS 28168 -- Mitsui Chemicals, Nihon Schering  
 MSH fusion toxin -- Ligand  
 MSI-99 -- Genæra  
 MT 201 -- Micromet  
 Muc-1 vaccine -- Corixa  
 mucosal tolerance -- Aberdeen  
 mullerian inhibiting subst  
 muplestim -- Genetics Institute, Novartis,  
 DSM Anti-Infectives  
 murine MAb -- KS Biomedix  
 Mutant somatropin -- JCR Pharmaceutical  
 MV 833 -- Toagosei  
 Mycoplasma pulmonis vaccine  
 Mycoprex -- XOMA  
 myeloperoxidase -- Henogen  
 myostatin -- Genetics Institute  
 Nacolomab tafanatox -- Pharmacia  
 Nagrecor -- Scios  
 nagrestipen -- British Biotech  
 NAP-5 -- Corvas Intl.  
 NAPc2 -- Corvas Intl.  
 nartograstim -- Kyowa  
 Natalizumab -- Protein Design Labs  
 Nateplase -- NIH, Nihon Schering  
 nateplase -- Schering AG  
 NBI-3001 -- Neurocrine Biosci.  
 NBI-5788 -- Neurocrine Biosci.  
 NBI-6024 -- Neurocrine Biosci.  
 Nef inhibitors -- BRI  
 Neisseria gonorrhoea vaccine -- Antex Biologics  
 Neomycin B-arginine conjugate  
 Nerelimomab -- Chiron  
 Nerve growth factor -- Amgen -- Chiron, Genentech  
 Nerve growth factor gene therapy  
 nesiritide citrate -- Scios  
 neuregulin-2 -- CeNeS  
 neurocan -- NYU  
 neuronal delivery system -- CAMR  
 Neurophil inhibitory Factor -- Corvas  
 Neuroprotective vaccine -- University of Auckland  
 neurotrophic chimaeras -- Regeneron  
 neurotrophic factor -- NsGene, CereMedix

FIG. 28U

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NeuroVax -- Immune Response  
 neurturnin -- Genentech  
 neutral endopeptidase -- Genentech  
 NGF enhancers -- NeuroSearch  
 NHL vaccine -- Large Scale Biology  
 NIP45 -- Boston Life Sciences  
 NKI-B20  
 NM 01 -- Nissin Food  
 NMI-139 -- NitroMed  
 NMMP -- Genetics Institute  
 NN-2211 -- Novo Nordisk  
 Noggin -- Regeneron  
 Nonacog alfa  
 Norelin -- Biostar  
 Norwalk virus vaccine  
 NRLU 10 -- NeoRx  
 NRLU 10 PE -- NeoRx  
 NT-3 -- Regeneron  
 NT-4/5 -- Genentech  
 NU 3056  
 NU 3076  
 NX 1838 -- Gilead Sciences  
 NY ESO-1/CAG-3 antigen -- NIH  
 NYVAC-7 -- Aventis Pasteur  
 NZ-1002 -- Novazyme  
 obesity therapy -- Nobex  
 OC 10426 -- Ontogen  
 OC 144093 -- Ontogen  
 OCIF -- Sankyo  
 Oct-43 -- Otsuka  
 Odulimomab -- Immunotech  
 OK PSA - liposomal  
 OKT3-gamma-1-ala-ala  
 OM 991  
 OM 992  
 Omalizumab -- Genentech  
 oncoimmunin-L -- NIH  
 Oncolysin B -- ImmunoGen  
 Oncolysin CD6 -- ImmunoGen  
 Oncolysin M -- ImmunoGen  
 Oncolysin S -- ImmunoGen  
 Oncophage -- Antigenics  
 Oncostatin M -- Bristol-Myers Squibb  
 OncoVax-CL -- Jenner Biotherapies  
 OncoVax-P -- Jenner Biotherapies  
 onercept -- Yeda  
 onychomycosis vaccine -- Boehringer  
 Ingelheim  
 opebecan -- XOMA  
 opioids -- Arizona  
 Oprelvekin -- Genetics Institute  
 Oregovomab -- AltaRex  
 Org-33408 b-- Akzo Nobel  
 Orlip DP -- EpiCept  
 oryzacystatin  
 OSA peptides -- GenSci Regeneration  
 osteoblast-cadherin GF -- Pharis  
 Osteocalcin-thymidine kinase gene therapy  
 osteogenic protein -- Curis  
 osteopontin -- OraPharma  
 osteoporosis peptides -- Integra, Telios  
 osteoprotegerin -- Amgen, SnowBrand  
 otitis media vaccines -- Antex Biologics  
 ovarian cancer -- University of Alabama  
 OX40-IgG fusion protein -- Cantab, Xenova  
 P 246 -- Diatide  
 P 30 -- Alfacell  
 p1025 -- Active Biotech  
 P-113<sup>A</sup> -- Demegen  
 P-16 peptide -- Transition Therapeutics  
 p43 -- Ramot  
 P-50 peptide -- Transition Therapeutics  
 p53 + RAS vaccine -- NIH, NCI  
 PACAP(1-27) analogue  
 paediatric vaccines -- Chiron  
 Pafase -- ICOS  
 PAGE-4 plasmid DNA -- IDEC  
 PAI-2 -- Biotech Australia, Human  
 Therapeutics  
 Palifermin (keratinocyte growth factor) --  
 Amgen  
 Palivizumab -- MedImmune

FIG. 28V



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PAM 4 -- Merck  
 pamiteplase -- Yamanouchi  
 pancreatin, Minitabs -- Eurand  
 Pangen -- Fournier  
 Pantarin -- Selective Genetics  
 Parainfluenza virus vaccine -- Pharmacia,  
 Pierre Fabre  
 paraoxanase -- Esperion  
 parathyroid hormone -- Abiogen, Korea  
 Green Cross  
 Parathyroid hormone (1-34) --  
 Chugai/Suntory  
 Parkinson's disease gene therapy -- Cell  
 Genesys/ Ceregene  
 Parvovirus vaccine -- MedImmune  
 PCP-Scan -- Immunomedics  
 PDGF -- Chiron  
 PDGF cocktail -- Theratechnologies  
 peanut allergy therapy -- Dynavax  
 PEG anti-ICAM MAb -- Boehringer  
 Ingelheim  
 PEG asparaginase -- Enzon  
 PEG glucocerebrosidase  
 PEG hirudin -- Knoll  
 PEG interferon-alpha-2a -- Roche  
 PEG interferon-alpha-2b + ribavirin --  
 Biogen, Enzon, ICN Pharmaceuticals,  
 Schering-Plough  
 PEG MAb A5B7 --  
 Pegacaristim -- Amgen -- Kirin Brewery --  
 ZymoGenetics  
 Pegaldesleukin -- Research Corp  
 pegaspargase -- Enzon  
 pegfilgrastim -- Amgen  
 PEG-interferon Alpha -- Viragen  
 PEG-interferon Alpha 2A -- Hoffman La-  
 Roche  
 PEG-interferon Alpha 2B -- Schering-  
 Plough  
 PEG-r-hirudin -- Abbott  
 PEG-rHuMGDF -- Amgen  
 PEG-uricase -- Mountain View  
 Pegvisomant -- Genentech  
 PEGylated proteins, PolyMASC -- Valentis  
 PEGylated recombinant native human leptin  
 -- Roche  
 Pentumomab  
 Penetratin -- Cyclacel  
 Pepscan -- Antisoma  
 peptide G -- Peptech, ICRT  
 peptide vaccine -- NIH ,NCI  
 Pexelizumab  
 pexiganan acetate -- Genaera  
 Pharmaprojects No. 3179 -- NYU  
 Pharmaprojects No. 3390 -- Ernest Orlando  
 Pharmaprojects No. 3417 -- Sumitomo  
 Pharmaprojects No. 3777 -- Acambis  
 Pharmaprojects No. 4209 -- XOMA  
 Pharmaprojects No. 4349 -- Baxter Intl.  
 Pharmaprojects No. 4651  
 Pharmaprojects No. 4915 -- Avanir  
 Pharmaprojects No. 5156 -- Rhizogenics  
 Pharmaprojects No. 5200 -- Pfizer  
 Pharmaprojects No. 5215 -- Origene  
 Pharmaprojects No. 5216 -- Origene  
 Pharmaprojects No. 5218 -- Origene  
 Pharmaprojects No. 5267 -- ML  
 Laboratories  
 Pharmaprojects No. 5373 -- MorphoSys  
 Pharmaprojects No. 5493 -- Metabolex  
 Pharmaprojects No. 5707 -- Genentech  
 Pharmaprojects No. 5728 -- Autogen  
 Pharmaprojects No. 5733 -- BioMarin  
 Pharmaprojects No. 5757 -- NIH  
 Pharmaprojects No. 5765 -- Gryphon  
 Pharmaprojects No. 5830 -- AntiCancer  
 Pharmaprojects No. 5839 -- Dyax  
 Pharmaprojects No. 5849 -- Johnson &  
 Johnson  
 Pharmaprojects No. 5860 -- Mitsubishi-  
 Tokyo

FIG. 28W

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- Pharmaprojects No. 5869 -- Oxford GlycoSciences
- Pharmaprojects No. 5883 -- Asahi Brewery
- Pharmaprojects No. 5947 -- StressGen
- Pharmaprojects No. 5961 -- Theratechnologies
- Pharmaprojects No. 5962 -- NIH
- Pharmaprojects No. 5966 -- NIH
- Pharmaprojects No. 5994 -- Pharming
- Pharmaprojects No. 5995 -- Pharming
- Pharmaprojects No. 6023 -- IMMUCON
- Pharmaprojects No. 6063 -- Cytoclonal
- Pharmaprojects No. 6073 -- SIDDCO
- Pharmaprojects No. 6115 -- Genzyme
- Pharmaprojects No. 6227 -- NIH
- Pharmaprojects No. 6230 -- NIH
- Pharmaprojects No. 6236 -- NIH
- Pharmaprojects No. 6243 -- NIH
- Pharmaprojects No. 6244 -- NIH
- Pharmaprojects No. 6281 -- Senetek
- Pharmaprojects No. 6365 -- NIH
- Pharmaprojects No. 6368 -- NIH
- Pharmaprojects No. 6373 -- NIH
- Pharmaprojects No. 6408 -- Pan Pacific
- Pharmaprojects No. 6410 -- Athersys
- Pharmaprojects No. 6421 -- Oxford GlycoSciences
- Pharmaprojects No. 6522 -- Maxygen
- Pharmaprojects No. 6523 -- Pharis
- Pharmaprojects No. 6538 -- Maxygen
- Pharmaprojects No. 6554 -- APALEXO
- Pharmaprojects No. 6560 -- Ardana
- Pharmaprojects No. 6562 -- Bayer
- Pharmaprojects No. 6569 -- Eos
- Phenoxazine
- Phenylase -- Ibbex
- Pigment epithelium derived factor -- plasminogen activator inhibitor-1, recombinant -- DuPont Pharmaceuticals
- Plasminogen activators -- Abbott Laboratories, American Home Products, Boehringer Mannheim, Chiron Corporation, DuPont Pharmaceuticals, Eli Lilly, Shionogi, Genentech, Genetics Institute, GlaxoSmithKline, Hemispherx Biopharma, Merck & Co, Novartis, Pharmacia Corporation, Wakamoto, Yeda
- plasminogen-related peptides -- Bio-Tech. General/MGH
- platelet factor 4 -- RepliGen
- Platelet-derived growth factor -- Amgen -- ZymoGenetics
- plusonemin -- Hayashibara
- PMD-2850 -- Protherics
- Pneumococcal vaccine -- Antex Biologics, Aventis Pasteur
- Pneumococcal vaccine intranasal -- BioChem Vaccines/Biovector
- PR1A3
- PR-39
- pralmorelin -- Kaken
- Pretarget-Lymphoma -- NeoRx
- Priliximab -- Centocor
- PRO 140 -- Progenics
- PRO 2000 -- Procept
- PRO 367 -- Progenics
- PRO 542 -- Progenics
- pro-Apo A-I -- Esperion
- prolactin -- Genzyme
- Prosaptide TX14(A) -- Bio-Tech. General
- prostate cancer antibodies -- Immunex, UroCor
- prostate cancer antibody therapy -- Genentech/UroGenesys, Genotherapeutics
- prostate cancer immunotherapeutics -- The PSMA Development Company
- prostate cancer vaccine -- Aventis Pasteur, Zonagen, Corixa, Dendreon, Jenner
- Biotherapies, Therion Biologics

FIG. 28X

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prostate-specific antigen -- Entremed  
 protein A -- RepliGen  
 protein adhesives -- Enzon  
 protein C -- Baxter Intl., PPL Therapeutics,  
     ZymoGenetics  
 protein C activator -- Gilead Sciences  
 protein kinase R antagonists -- NIH  
 protirelin -- Takeda  
 protocadherin 2 -- Caprion  
 Pro-urokinase -- Abbott, Bristol-Myers  
     Squibb, Dainippon, Tosoh -- Welfide  
 P-selectin glycoprotein ligand-1 -- Genetics  
     Institute  
 pseudomonal infections -- InterMune  
 Pseudomonas vaccine -- CytoVax  
 PSGL-Ig -- American Home Products  
 PSP-94 -- Procyon  
 PTH 1-34 -- Nobex  
 Quilimmune-M -- Antigenics  
 R 744 -- Roche  
 R 101933  
 R 125224 -- Sankyo  
 RA therapy -- Cardion  
 Rabies vaccine recombinant -- Aventis  
     Pasteur, BioChem Vaccines, Kaketsuken  
     Pharmaceuticals  
 RadioTheraCIM -- YM BioSciences  
 Ramot project No. 1315 -- Ramot  
 Ramot project No. K-734A -- Ramot  
 Ramot project No. K-734B -- Ramot  
 Ranibizumab (Anti-VEGF fragment) --  
     Genentech  
 RANK -- Immunex  
 ranpirinase -- Alfacell  
 ranpirinase-anti-CD22 MAb -- Alfacell  
 RANTES inhibitor -- Milan  
 RAPID drug delivery systems -- ARIAD  
 rasburicase -- Sanofi  
 rBPI-21, topical -- XOMA  
 RC 529 -- Corixa  
 rCFTR -- Genzyme Transgenics

RD 62198  
 rDnase -- Genentech  
 RDP-58 -- SangStat  
 ReceptTox-Fce -- Keryx  
 ReceptTox-GnRH -- Keryx, MTR  
     Technologies  
 ReceptTox-MBP -- Keryx, MTR  
     Technologies  
 recFSH -- Akzo Nobel, Organon  
 REGA 3G12  
 Regavirumab -- Teijin  
 relaxin -- Connetics Corp  
 Renal cancer vaccine -- MacroPharm  
 repifermin -- Human Genome Sciences  
 Respiratory syncytial virus PFP-2 vaccine --  
     Wyeth-Lederle  
 Respiratory syncytial virus vaccine --  
     GlaxoSmithKline, Pharmacia, Pierre Fabre  
 Respiratory syncytial virus vaccine  
     inactivated  
 Respiratory syncytial virus-parainfluenza  
     virus vaccine -- Aventis Pasteur,  
     Pharmacia  
 Reteplase -- Boehringer Mannheim,  
     Hoffman La-Roche  
 Retropep -- Retroscreen  
 RFB4 (dsFv) PE38  
 RFI 641 -- American Home Products  
 RFTS -- UAB Research Foundation  
 RG 12986 -- Aventis Pasteur  
 RG 83852 -- Aventis Pasteur  
 RG-1059 -- RepliGen  
 rGCR -- NIH  
 rGLP-1 -- Restoragen  
 rGRF -- Restoragen  
 rh Insulin -- Eli Lilly  
 RHAMM targeting peptides -- Cangene  
 rHb1.1 -- Baxter Intl.  
 rhCC10 -- Claragen  
 rhCG -- SeroNo  
 Rheumatoid arthritis gene therapy

FIG. 28Y

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Rheumatoid arthritis vaccine -- Veterans

Affairs Medical Center

rhLH -- Serono

Ribozyme gene therapy -- Genset

Rickettsial vaccine recombinant

RIGScan CR -- Neoprobe

RIP-3 -- Rigel

Rituximab -- Genentech

RK-0202 -- RxKinetix

RLT peptide -- Esperion

rM/NEI -- IVAX

rmCRP -- Immtech

RN-1001 -- Renovo

RN-3 -- Renovo

RNase conjugate -- Immunomedics

RO 631908 -- Roche

Rotavirus vaccine -- Merck

RP 431 -- DuPont Pharmaceuticals

RP-128 -- Resolution

RPE65 gene therapy --

RPR 110173 -- Aventis Pasteur

RPR 115135 -- Aventis Pasteur

RPR 116258A -- Aventis Pasteur

rPSGL-Ig -- American Home Products

r-SPC surfactant -- Byk Gulden

RSV antibody -- Medimmune

Ruplizumab -- Biogen

rV-HER-2/neu -- Therion Biologics

SA 1042 -- Sankyo

sacrosidase -- Orphan Medical

Sant 7

Sargramostim -- Immunex

saruplase -- Gruenenthal

Satumomab -- Cytogen

SB 1 -- COR Therapeutics

SB 207448 -- GlaxoSmithKline

SB 208651 -- GlaxoSmithKline

SB 240683 -- GlaxoSmithKline

SB 249415 -- GlaxoSmithKline

SB 249417 -- GlaxoSmithKline

SB 6 -- COR Therapeutics

SB RA 31012 --

SC 56929 -- Pharmacia

SCA binding proteins -- Curis, Enzon

scFv(14E1)-ETA Berlex Laboratories,

Schering AG

ScFv(FRP5)-ETA --

ScFv6C6-PE40 --

SCH 55700 -- Celltech

Schistosomiasis vaccine -- Glaxo

Wellcome/Medeva, Brazil

SCPF -- Advanced Tissue Sciences

scuPA-suPAR complex -- Hadasit

SD-9427 -- Pharmacia

SDF-1 -- Ono

SDZ 215918 -- Novartis

SDZ 280125 -- Novartis

SDZ 89104 -- Novartis

SDZ ABL 364 -- Novartis

SDZ MMA 383 -- Novartis

Secretin -- Ferring, Repligen

serine protease inhbs -- Pharis

sermorelin acetate -- Sero

SERP-1 -- Viron

sertenef -- Dainippon

serum albumin, Recombinant human --

Aventis Behring

serum-derived factor -- Hadasit

Sevirumab -- Novartis

SGN 14 -- Seattle Genetics

SGN 15 -- Seattle Genetics

SGN 17/19 -- Seattle Genetics

SGN 30 -- Seattle Genetics

SGN-10 -- Seattle Genetics

SGN-11 -- Seattle Genetics

SH 306 -- DuPont Pharmaceuticals

Shanvac-B -- Shantha

Shigella flexneri vaccine -- Avant, Acambis,

Novavax

Shigella sonnei vaccine --

sICAM-1 -- Boehringer Ingelheim

Silteplase -- Genzyme

FIG. 28Z

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SIV vaccine -- Endocon, Institut Pasteur  
 SK 896 -- Sanwa Kagaku Kenkyusho  
 SK-827 -- Sanwa Kagaku Kenkyusho  
 Skeletex -- CellFactors  
 SKF 106160 -- GlaxoSmithKline  
 S-nitroso-AR545C --  
 SNTP -- Active Biotech  
 somatomedin-1 -- GroPep, Mitsubishi-  
 Tokyo, NIH  
 somatomedin-1 carrier protein -- Insmed  
 somatostatin -- Ferring  
 Somatotropin/  
 Human Growth Hormone -- Bio-Tech.  
 General, Eli Lilly  
 somatropin -- Bio-Tech. General, Alkermes,  
 ProLease, Aventis Behring, Biovector,  
 Cangene, Dong-A, Eli Lilly, Emisphere,  
 Enact, Genentech, Genzyme Transgenics,  
 Grandis/InfiMed, CSL, InfiMed, MacroMed,  
 Novartis, Novo Nordisk, Pharmacia  
 Serono, TranXenoGen  
 somatropin derivative -- Schering AG  
 somatropin, AIR -- Eli Lilly  
 Somatropin, inhaled -- Eli Lilly/Alkermes  
 somatropin, Kabi -- Pharmacia  
 somatropin, Orasome -- Novo Nordisk  
 Sonermin -- Daiippon Pharmaceutical  
 SP(V5.2)C -- Supertek  
 SPf66  
 sphingomyelinase -- Genzyme  
 SR 29001 -- Sanofi  
 SR 41476 -- Sanofi  
 SR-29001 -- Sanofi  
 SS1(dsFV)-PE38 -- NeoPharm  
 $\beta$ 2 microglobulin -- Avidex  
 $\beta$ 2-microglobulin fusion proteins -- NIH  
 $\beta$ -amyloid peptides -- CeNeS  
 $\beta$ -defensin -- Pharis  
 Staphylococcus aureus infections --  
 Inhibibex/ZLB  
 Staphylococcus aureus vaccine conjugate --  
 Nabi  
 Staphylococcus therapy -- Tripep  
 Staphylokinase -- Biovation, Prothera,  
 Thrombogenetics  
 Streptococcal A vaccine -- M6  
 Pharmaceuticals, North American Vaccine  
 Streptococcal B vaccine -- Microscience  
 Streptococcal B vaccine recombinant --  
 Biochem Vaccines  
 Streptococcus pyogenes vaccine  
 STRL-33 -- NIH  
 Subalin -- SRC VB VECTOR  
 SUIIS -- United Biomedical  
 SUIIS-LHRH -- United Biomedical  
 SUN-E3001 -- Suntory  
 super high affinity monoclonal antibodies --  
 YM BioSciences  
 Superoxide dismutase -- Chiron, Enzon,  
 Ube Industries, Bio-Tech, Yeda  
 superoxide dismutase-2 -- OXIS  
 suppressin -- UAB Research Foundation  
 SY-161-P5 -- ThromboGenics  
 SY-162 -- ThromboGenics  
 Systemic lupus erythematosus vaccine --  
 MedClone/VivoRx  
 T cell receptor peptides -- Xoma  
 T cell receptor peptide vaccine  
 T4N5 liposomes -- AGI Dermatics  
 TACI, soluble -- ZymoGenetics  
 targeted apoptosis -- Antisoma  
 tasonermin -- Boehringer Ingelheim  
 TASP  
 TASP-V  
 Tat peptide analogues -- NIH  
 TBP I -- Yeda  
 TBP II  
 TBV25H -- NIH  
 Tc 99m ior cea1 -- Center of Molecular  
 Immunology  
 Tc 99m P 748 -- Diatide

FIG. 28AA

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Tc 99m votumab -- Intracell  
 Tc-99m rh-Annexin V -- Theseus Imaging  
 teceleukin -- Biogen  
 tenecteplase -- Genentech  
 Teriparatide -- Armour Pharmaceuticals,  
     Asahi Kasei, Eli Lilly  
 terlipressin -- Ferring  
 testisin -- AMRAD  
 Tetra fibrin -- Roche  
 TFPI -- EntrelMed  
 tgD-IL-2 -- Takeda  
 TGF-Alpha -- ZymoGenetics  
 TGF- $\beta$  -- Kolon  
 TGF- $\beta$ 2 -- Insmed  
 TGF- $\beta$ 3 -- OSI  
 Thalassemia gene therapy -- Crucell  
 TheraCIM-h-R3 -- Center of Molecular  
     Immunology, YM BioSciences  
 Theradigm-HBV -- Epimmune  
 Theradigm-HPV -- Epimmune  
 Theradigm-malaria -- Epimmune  
 Theradigm-melanoma -- Epimmune  
 TheraFab -- Antisoma  
 ThGRF 1-29 -- Theratechnologies  
 ThGRF 1-44 -- Theratechnologies  
 Thrombin receptor activating peptide --  
     Abbott  
 thrombomodulin -- Iowa, Novocastra  
 Thrombopoietin -- Dragon Pharmaceuticals,  
     Genentech  
 thrombopoietin, Pliva -- Recepton  
 Thrombospondin 2 --  
 thrombostatin -- Thromgen  
 thymalfasin -- SciClone  
 thymocartin -- Gedeon Richter  
 thymosin Alpha1 -- NIH  
 thyroid stimulating hormone -- Genzyme  
 tICAM-1 -- Bayer  
 Tick anticoagulant peptide -- Merck  
 TIF -- Xoma  
 Tifacogin -- Chiron, NIS, Pharmacia  
 Tissue factor -- Genentech  
 Tissue factor pathway inhibitor  
 TJN-135 -- Tsumura  
 TM 27 -- Avant  
 TM 29 -- Avant  
 TMC-151 -- Tanabe Seiyaku  
 TNF tumour necrosis factor -- Asahi Kasei  
 TNF Alpha -- CytImmune  
 TNF antibody -- Johnson & Johnson  
 TNF binding protein -- Amgen  
 TNF degradation product -- Oncotech  
 TNF receptor -- Immunex  
 TNF receptor 1, soluble -- Amgen  
 TNF Tumour necrosis factor-alpha -- Asahi  
     Kasei, Genentech, Mochida  
 TNF-Alpha inhibitor -- Tripep  
 TNFR:Fc gene therapy -- Targeted Genetics  
 TNF-SAM2  
 Tolerimab -- Innogenetics  
 Toxoplasma gondii vaccine --  
     GlaxoSmithKline  
 TP 9201 -- Telios  
 TP10 -- Avant  
 TP20 -- Avant  
 tPA -- Centocor  
 trafermin -- Scios  
 TRAIL/Apo2L -- Immunex  
 TRAIL-R1 MAb -- Cambridge Antibody  
     Technologies  
 transferrin-binding proteins -- CAMR  
 Transforming growth factor-beta-1 --  
     Genentech  
 transport protein -- Genesis  
 Trastuzumab -- Genentech  
 TRH -- Ferring  
 Triabin -- Schering AG  
 Triconal  
 Triflavin  
 troponin I -- Boston Life Sciences  
 TRP-2<sup>A</sup> -- NIH  
 trypsin inhibitor -- Mochida

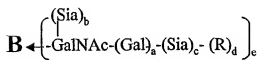
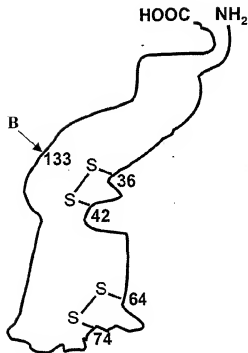
FIG. 28BB

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<p>TSP-1 gene therapy –  TT-232  TTS-CD2 -- Active Biotech  Tuberculosis vaccine -- Aventis Pasteur, Genesis  Tumor Targeted Superantigens -- Active Biotech -- Pharmacia  tumour vaccines -- PhotoCure  tumour-activated prodrug antibody conjugates -- Millennium/ImmunoGen  tumstatin -- ILEX  Tuvirumab -- Novartis  TV-4710 -- Teva  TWEAK receptor -- Immunex  TXU-PAP  TY-10721 -- TOA Eiyo  Type I diabetes vaccine -- Research Corp  Typhoid vaccine CVD 908  U 143677 -- Pharmacia  U 81749 -- Pharmacia  UA 1248 -- Arizona  UGIF -- Sheffield  UIC 2  UK 101  UK-279276 -- Corvas Intl.  urodilatin -- Pharis  urofollitrophin -- Serono  Urokinase -- Abbott  uteroferrin-- Pepgen  V 20 -- GLYCODesign  V2 vasopressin receptor gene therapy vaccines -- Active Biotech  Varicella zoster glycoprotein vaccine -- Research Corporation Technologies  Varicella zoster virus vaccine live -- Cantab Pharmaceuticals  Vascular endothelial growth factor -- Genentech, University of California</p>	<p>Vascular endothelial growth factors -- R&amp;D Systems  vascular targeting agents -- Peregrine  vasopermeation enhancement agents -- Peregrine  vasostatin -- NIH  VCL -- Bio-Tech. General  VEGF -- Genentech, Scios  VEGF inhibitor -- Chugai  VEGF-2 -- Human Genome Sciences  VEGF-Trap -- Regeneron  viscumin, recombinant -- Madaus  Vitaxin  Vitraxe -- ISTA Pharmaceuticals  West Nile virus vaccine -- Bavarian Nordic  WP 652  WT1 vaccine -- Corixa  WX-293 -- Wilex BioTech.  WX-360 -- Wilex BioTech.  WX-UK1 -- Wilex BioTech.  XMP-500 -- XOMA  XomaZyme-791 -- XOMA  XTL 001 -- XTL Biopharmaceuticals  XTL 002 -- XTL Biopharmaceuticals  yeast delivery system -- GlobelImmune  Yersinia pestis vaccine  YIGSR-Stealth -- Johnson &amp; Johnson  Yissum Project No. D-0460 -- Yissum  YM 207 -- Yamanouchi  YM 337 -- Protein Design Labs  Yttrium-90 labelled biotin  Yttrium-90-labeled anti-CEA MAb T84.66 -- ZD 0490 -- AstraZeneca  ziconotide -- Elan  ZK 157138 -- Berlex Laboratories  Zolimomab arixox  Zorcell -- Immune Response  ZRXL peptides -- Novartis</p>
---	---

FIG. 28CC

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a-c, e (independently selected) = 0 or 1;

d = 0;

R = modifying group, sialyl or oligosialyl

FIG. 29A



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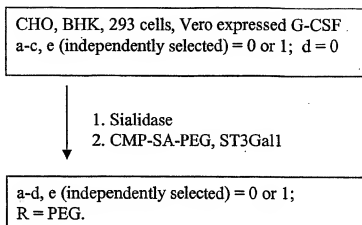


FIG. 29B

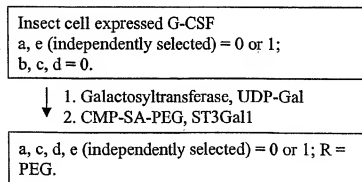


FIG. 29C

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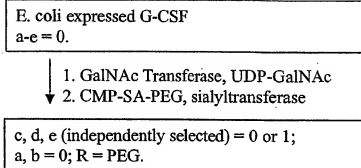


FIG. 29D

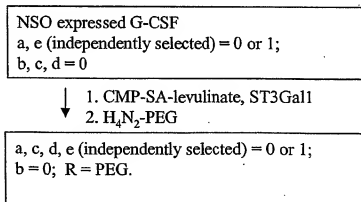


FIG. 29E

63/498

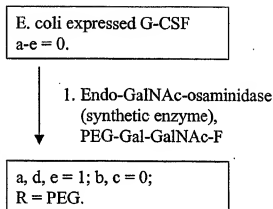


FIG. 29F

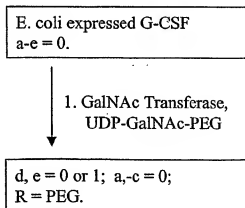
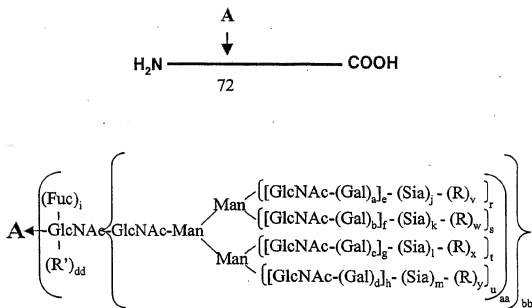


FIG. 29G

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a-d, i, n-u (independently selected) = 0 or 1.

aa, bb, cc, dd, ee (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group,

glycoconjugate.

FIG. 30A

65/498

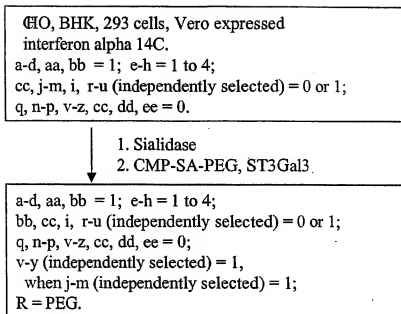


FIG. 30B

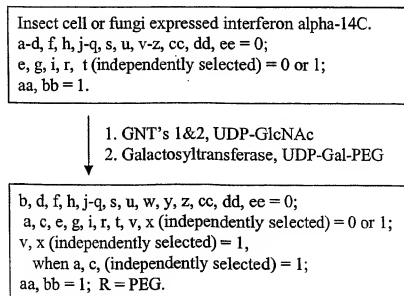


FIG. 30C

66/498

Yeast expressed interferon alpha-14C.

a-q, cc, dd, ee, v-z = 0;

r-y (independently selected) = 0 to 1;

aa, bb = 1;

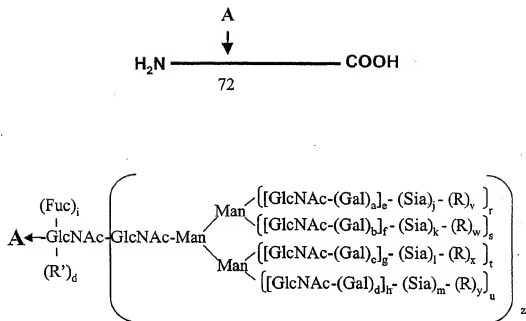
R (branched or linear) = Man, oligomannose or polysaccharide.

- ↓
1. Endo-H
  2. Galactosyltransferase, UDP-Gal
  3. CMP-SA-PEG, ST3Gal3

a-z, bb = 0; aa = 1; R' = -Gal-Sia-PEG.

FIG. 30D

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1.

R = polymer; R' = sugar, glycoconjugate.

FIG. 30E

68/498

CHO, BHK, 293 cells, Vero expressed  
interferon alpha-14C.

h = 1 to 3;

a-g, j-m, i (independently selected) = 0 or 1;

r-u (independently selected) = 0 or 1;

n, v-y = 0; z = 1.



1. CMP-SA-PEG, ST3Gal3

h = 1 to 3;

a-g, i (independently selected) = 0 or 1;

r-u (independently selected) = 0 or 1;

j-m, v-y (independently selected) = 0 or 1;

z = 1; n = 0; R = PEG.

FIG. 30F

Insect cell or fungi expressed  
interferon alpha-14C.

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, r, t (independently selected) = 0 or 1;

z = 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;

z = 1; n = 0; R = PEG.

FIG. 30G



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Yeast expressed interferon alpha-14C.  
a-n = 0; r-y (independently selected) = 0 to 1;  
z = 1; R (branched or linear) = Man,  
oligomannose.

- ↓
1. mannosidases
  2. GNT's 1,2,4,5, UDP-GlcNAc
  3. Galactosyltransferase, UDP-Gal
  - 4.. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;  
z = 1; n = 0; R = PEG.

FIG. 30H

NSO expressed interferon alpha 14C.  
a-i, r-u (independently selected) = 0 or 1;  
j-m, n, v-y = 0; z = 1.

- ↓
1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt
  2.  $H_4N_2$ -PEG

a-i, j-m, r-y (independently selected) = 0 or 1;  
n = 0; z = 1; R = PEG.

FIG. 30I

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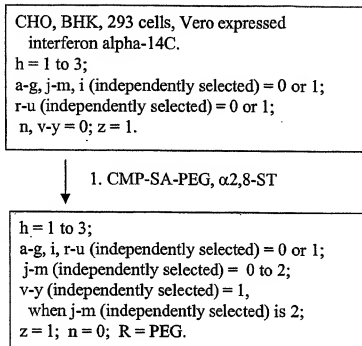


FIG. 30J

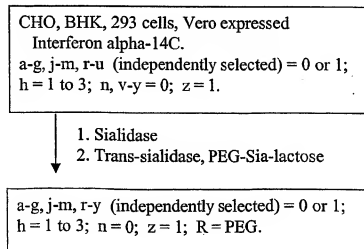


FIG. 30K

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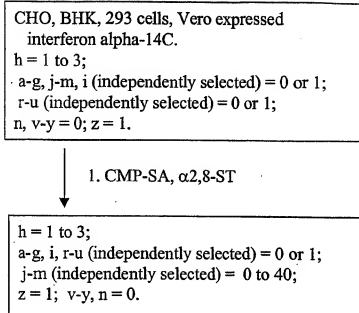


FIG. 30L

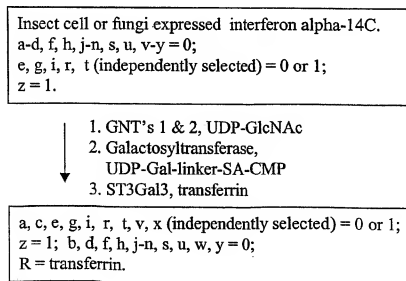


FIG. 30M

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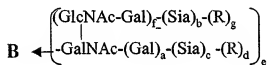
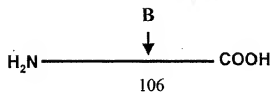
Insect cell or fungi expressed interferon alpha-14C.  
a-d, f, h, j-n, s, u, v-y = 0;  
e, g, i, r, t (independently selected) = 0 or 1; z = 1.

- ↓
1. endoglycanase
  2. Galactosyltransferase,  
UDP-Gal-linker-SA-CMP
  3. ST3Gal3, transferrin

i (independently selected) = 0 or 1;  
a-h, j-m, r-z = 0;  
n = 1; R' = -Gal-linker-transferrin.

FIG. 30N

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a-c, e, f (independently selected) = 0 or 1;  
 d, g = 0; R = polymer, glycoconjugate.

FIG. 300

74/498

CHO, BHK, 293 cells, Vero expressed  
IF-alpha (2a or 2b).  
a-c (independently selected) = 0 or 1;  
e = 1; d, f, g = 0

- ↓
1. Sialidase
  2. CMP-SA-PEG, ST3Gal1

a-d (independently selected) = 0 or 1;  
e = 1; b, f, g = 0; R = PEG.

FIG. 30P

Insect cell expressed interferon alpha (2a or 2b).  
a, e (independently selected) = 0 or 1;  
b, c, d, f, g = 0.

- ↓
1. Galactosyltransferase, UDP-Gal
  2. CMP-SA-PEG, ST3Gal1

a, c, d, e (independently selected) = 0 or 1;  
b, f, g = 0; R = PEG.

FIG. 30Q

75/498

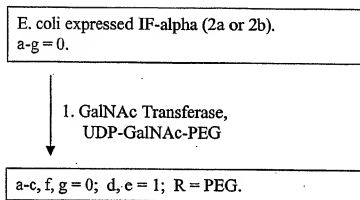


FIG. 30R

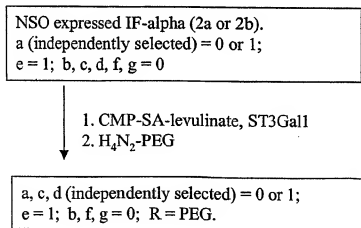


FIG. 30S

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E. coli expressed IF-alpha (2a or 2b).  
a-g = 0.



1. Endo-N-acetylgalactosamidase  
(synthetic enzyme),  
PEG-Gal-GalNAc-F

a, d, e = 1; b, c, f, g = 0; R = PEG.

FIG. 30T

E. coli expressed IF-alpha (2a or 2b).  
a-g = 0.



1. GalNAc Transferase, UDP-GalNAc  
2. sialyltransferase, CMP-SA-PEG

b, d = 0 or 1; e = 1; a, c, f, g = 0; R = PEG.

FIG. 30U



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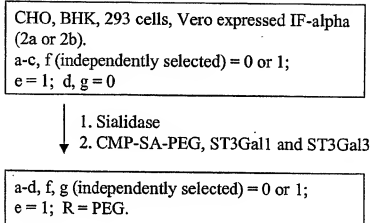


FIG. 30V

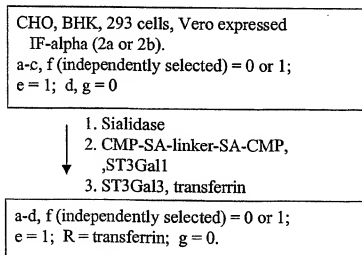
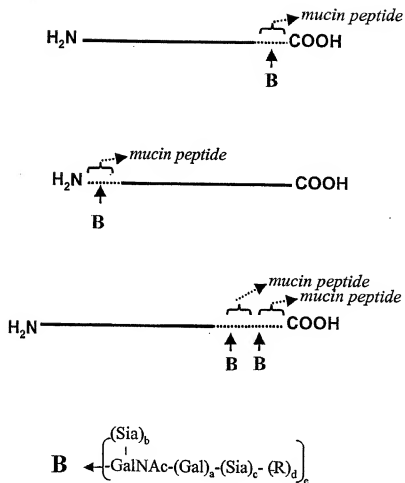


FIG. 30W

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a-c, e (independently selected) = 0 or 1;  
 d = 0; R = polymer, glycoconjugate.

FIG. 30X

79/498

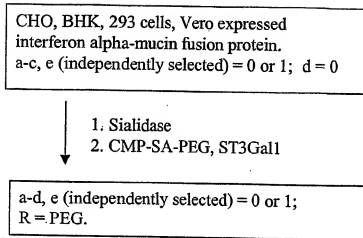


FIG. 30Y

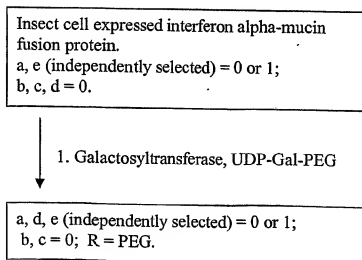


FIG. 30Z

80/498

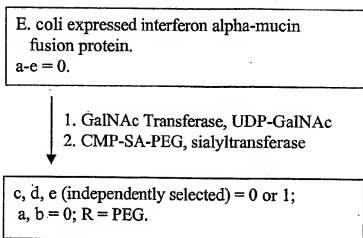
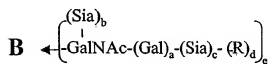
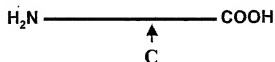
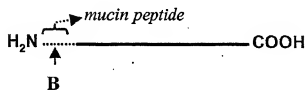
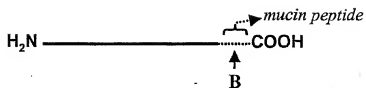


FIG. 30AA

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a-c, e (independently selected) = 0 or 1;  
d = 0; R = polymer, linker.

FIG. 30BB

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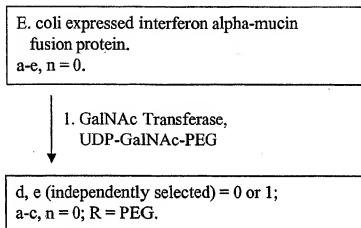


FIG. 30CC

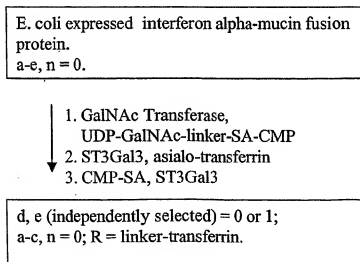


FIG. 30DD

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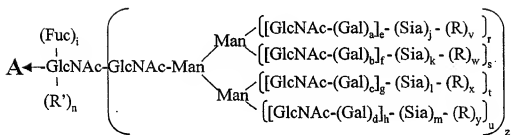
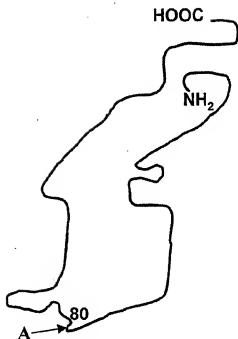
E. coli expressed Interferon alpha (no fusion).  
a-e, n = 0.

1. NHS-CO-linker-SA-CMP  
2. ST3Gal3, transferrin

a-e = 0; n = 1; R' = linker-transferrin.

FIG. 30EE

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1; R = polymer

FIG. 31A



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CHO, BHK, 293 cells, Vero expressed IF-beta  
 h = 1 to 3;  
 a-g, j-m, i (independently selected) = 0 or 1;  
 r-u (independently selected) = 0 or 1;  
 n, v-y = 0; z = 1.

- ↓
1. Sialidase
  2. CMP-SA-PEG, ST3Gal3

h = 1 to 3;  
 a-g, i (independently selected) = 0 or 1;  
 r-u (independently selected) = 0 or 1;  
 j-m, v-y (independently selected) = 0 or 1;  
 z = 1; n = 0; R = PEG.

FIG. 31B

Insect cell expressed IF-beta  
 a-d, f, h, j-n, s, u, v-y = 0;  
 e, g, i, r, t (independently selected) = 0 or 1;  
 z = 1.

- ↓
1. GNT's 1&2, UDP-GlcNAc
  2. Galactosyltransferase, UDP-Gal
  3. CMP-SA-PEG, ST3Gal3,  
buffer, salt

b, d, f, h, k, m, n, s, u, w, y = 0;  
 a, c, e, g, i, r, t (independently selected) = 0 or 1;  
 j, l, v, x (independently selected) = 0 or 1;  
 z = 1; R = PEG.

FIG. 31C

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Yeast expressed IF-beta  
 a-n = 0; z = 1;  
 r-y (independently selected) = 0 to 1;  
 R (branched or linear) = Man, oligomannose or  
 polysaccharide.

- ↓ 1. Endo-H  
 2. Galactosyltransferase, UDP-Gal  
 3.. CMP-SA-PEG, ST3Gal3

a-m, r-z= 0; n = 1; R' = -Gal-Sia-PEG.

FIG. 31D

CHO, BHK, 293 cells, Vero expressed IF-beta  
 h = 1 to 3;  
 a-g, j-m, i (independently selected) = 0 or 1;  
 r-u (independently selected) = 0 or 1;  
 n, v-y = 0; z = 1.

- ↓ 1. CMP-SA-PEG, ST3Gal3

h = 1 to 3;  
 a-g, i (independently selected) = 0 or 1;  
 r-u (independently selected) = 0 or 1;  
 j-m, v-y (independently selected) = 0 or 1;  
 z = 1; n = 0; R = PEG.

FIG. 31E

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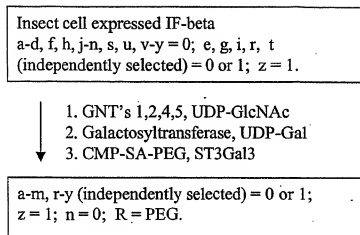


FIG. 31F

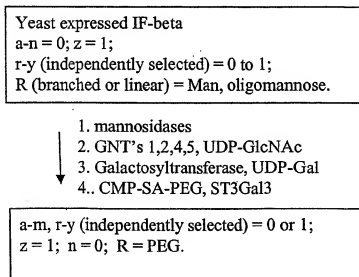


FIG. 31G

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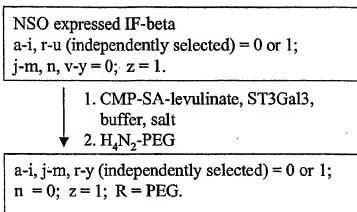


FIG. 31H

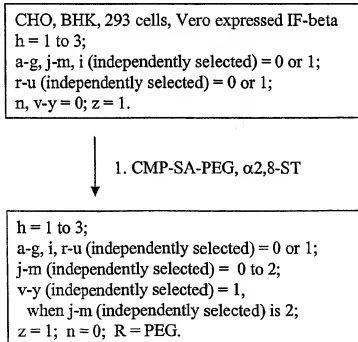


FIG. 31I

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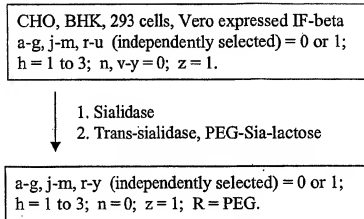


FIG. 31J

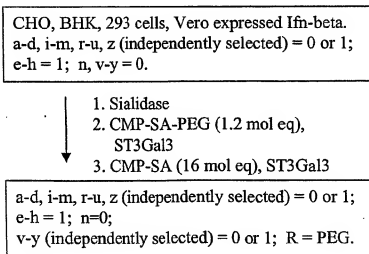


FIG. 31K

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NSO expressed Ifn-beta.

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and  $\alpha$ -galactosidase
  2.  $\alpha$ -Galactosyltransferase, UDP-Gal
  - ▼ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; R = PEG

n = 0; v-y (independently selected) = 1,  
when j-m (independently selected) is 1;

FIG. 31L

CHO, BHK, 293 cells, Vero expressed Ifn-beta.

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3
  3. CMP-SA, ST3Gal3

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n = 0;

v-y (independently selected) = 0 or 1; R = PEG.

FIG. 31M

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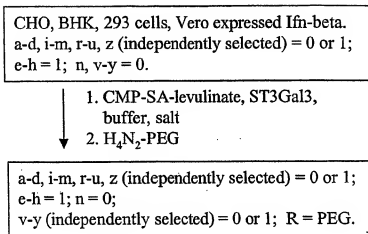


FIG. 31N

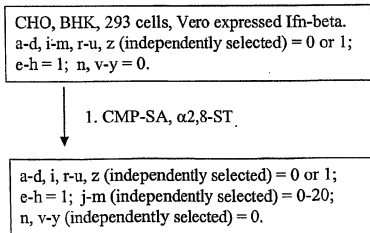


FIG. 31O





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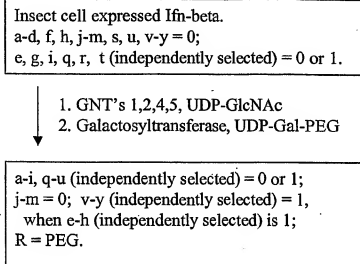


FIG. 31Q

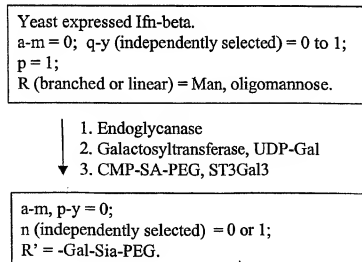


FIG. 31R

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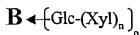
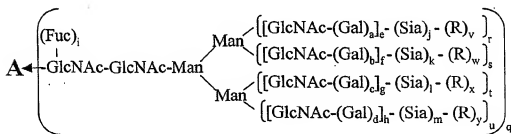
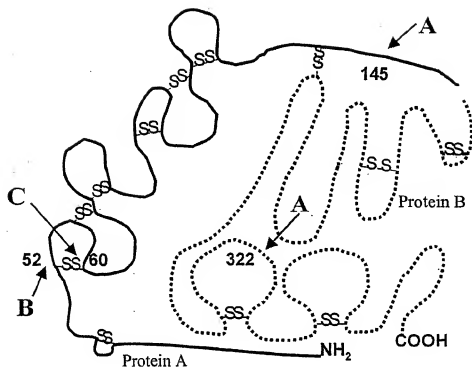
CHO, BHK, 293 cells, Vero expressed Ifn-beta.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP,  
ST3Gal3
  2. ST3Gal3, desialylated transferrin.
  3. CMP-SA, ST3Gal3

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0;  
v-y (independently selected) = 0 or 1;  
R = linker-transferrin.

FIG. 31S

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a-d, i, q-u (independently selected) = 0 or 1.

o, p (independently selected) = 0 or 1.

e-h, n (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-y = 0;

R = modifying group, mannose, oligo-mannose, Sia-Lewis X, Sia-Lewis A..

FIG. 32A

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BHK expressed Factor VII or VIIa

a-d, e, i, g, q, j, l, o, p (independently selected) = 0 or 1;  
r, t = 1; f, h, k, m, s, u, v-y = 0; n = 0-4.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mole eq),  
ST3Gal3

a-d, e, g, i, q, j, l, o, p (independently selected) = 0 or 1;  
r, t = 1; f, h, k, m, s, u, w, y = 0; n = 0-4;  
v, x, (independently selected) = 1,  
when j, l (respectively, independently selected) is 1;  
R = PEG.

FIG. 32B

CHO, BHK, 293 cells, Vero expressed Factor VII or VIIa

a-d, e, i, g, q, j, l, o, p (independently selected) = 0 or 1;  
r, t = 1; f, h, k, m, s, u, v-y = 0; n = 0-4.

- ↓
1. Sialidase
  2. CMP-SA-PEG (1.2 mole eq),  
ST3Gal3
  3. CMP-SA (8 mol eq), ST3Gal3

a-d, e, g, i, q, j, l, o, p (independently selected) = 0 or 1;  
r, t = 1; f, h, k, m, s, u, w, y = 0; n = 0-4;  
v or x, (independently selected) = 1,  
when j or l, (respectively, independently selected) is 1;  
R = PEG.

FIG. 32C

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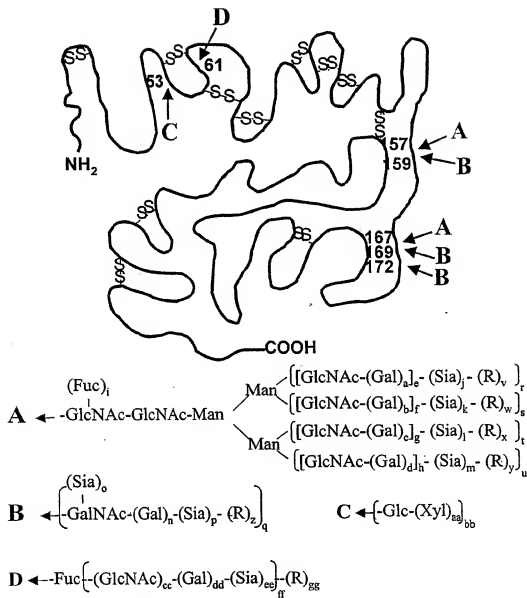
NSO expressed Factor VII or VIIa  
a--u (independently selected) = 0 or 1;  
v-y = 0; n = 0-4;  
Sia (independently selected) = Sia or Gal.

- ↓  
1. Sialidase and  $\alpha$ -galactosidase  
2. Galactosyltransferase, UDP-Gal  
▼ 3. CMP-SA-PEG, ST3Gal3

a-m, o-u (independently selected) = 0 or 1;  
n = 0-4; v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
Sia = Sia; R = PEG.

FIG. 32D

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a-d, i, n-u (independently selected) = 0 or 1.

bb, cc, dd, ee, ff, gg (independently selected) = 0 or 1.

e-h, aa (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = modifying group, mannose, oligo-mannose.

FIG. 33A

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CHO, BHK, 293 cells, Vero expressed Factor IX  
 a-d, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently  
 selected) = 0 or 1;  
 v-z, gg = 0.

1. Sialidase
2. CMP-SA-PEG, ST3Gal3

a-d, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)  
 = 0 or 1;  
 o, p, z = 0;  
 j-m, ee, v-y, gg (independently selected) = 0 or 1;  
 R = PEG.

FIG. 33B

CHO, BHK, 293 cells, Vero expressed Factor IX  
 a-d, n, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, j-m, i, o, p, r-u (independently  
 selected) = 0 or 1;  
 v-z, gg = 0.

1. Sialidase
2. CMP-SA-PEG, ST3Gal3
3. ST3Gal1, CMP-SA

a-d, n, p, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, i, r-u (independently selected) =  
 0 or 1;  
 j-m, ee, v-y, gg (independently selected) = 0 or 1;  
 o, z = 0; R = PEG.

FIG. 33C

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CHO, BHK, 293 cells, Vero expressed Factor IX  
 a-d, n, q, bb, cc, dd, ff = 1; e-h, aa = 1 to 4; ee, j-m, i,  
 o, p, r-u (independently selected) = 0 or 1; v-z, gg = 0.

- ↓
1. sialidase
  2. Galactosyltransferase, UDP-Gal
  3. CMP-SA, ST3Gal3
  4. CMP-SA-PEG, ST3Gal1

a-d, n, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, i, r-u (independently selected) =  
 0 or 1; R = PEG;  
 o, v-y, gg = 0;  
 j-m, p, ee (independently selected) = 0 or 1, but when  
 p = 1, z = 1.

FIG. 33D

CHO, BHK, 293 cells, Vero expressed Factor IX  
 a-d, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently  
 selected) = 0 or 1;  
 v-z, gg = 0.

- ↓
- CMP-SA-PEG, ST3Gal3

a-d, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)  
 = 0 or 1; R = PEG;  
 o, p, z = 0; j-m, ee, v-y, gg (independently selected) =  
 0 or 1.

FIG. 33E



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CHO, BHK, 293 cells, Vero expressed Factor IX  
 a-d, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently  
 selected) = 0 or 1;  
 v-z, gg = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt
  2. H<sub>4</sub>N<sub>2</sub>-PEG

a-d, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)  
 = 0 or 1;  
 o, p, z = 0; R = PEG;  
 j-m, ee, v-y, gg (independently selected) = 0 or 1.

FIG. 33F

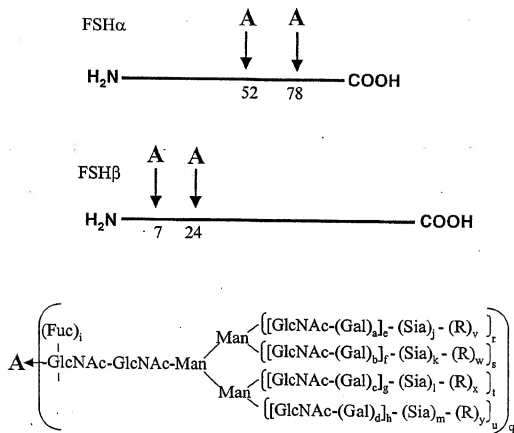
CHO, BHK, 293 cells, Vero expressed Factor IX  
 a-d, n, q, bb, cc, dd, ff = 1;  
 e-h, aa = 1 to 4;  
 ee, j-m, i, o, p, r-u (independently selected) = 0 or 1;  
 v-z, gg = 0.

- ↓
1. CMP-SA-PEG,  $\alpha$ 2,8-ST

a-d, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)  
 = 0 or 1;  
 o, p, z = 0; R = PEG;  
 j-m, ee (independently selected) = 0 to 2;  
 v-y, gg (independently selected) = 1, when j-m  
 (independently selected) is 2;

FIG. 33G

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose.

FIG. 34A

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CHO, BHK, 293 cells, Vero expressed FSH.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (16 mol eq),  
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = PEG.

FIG. 34B

CHO, BHK, 293 cells, Vero expressed FSH.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (1.2 mol eq),  
ST3Gal3
3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 34C

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NSO expressed FSH.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and  $\alpha$ -galactosidase
  2. Galactosyltransferase, UDP-Gal
  - ▼ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 34D

CHO, BHK, 293 cells, Vero expressed FSH.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3
  - ▼ 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 34E

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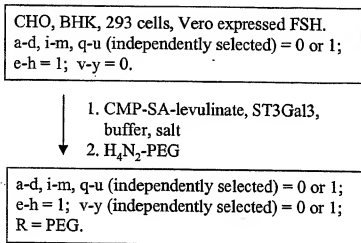


FIG. 34F

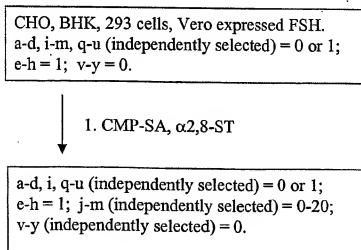


FIG. 34G

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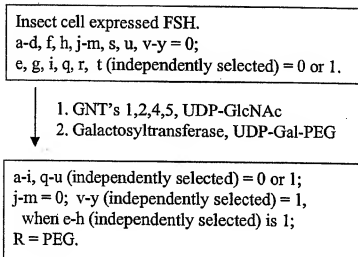


FIG. 34H

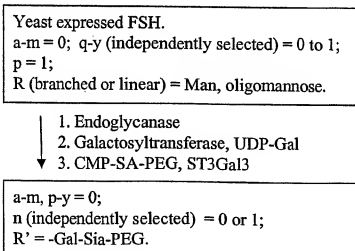


FIG. 34I

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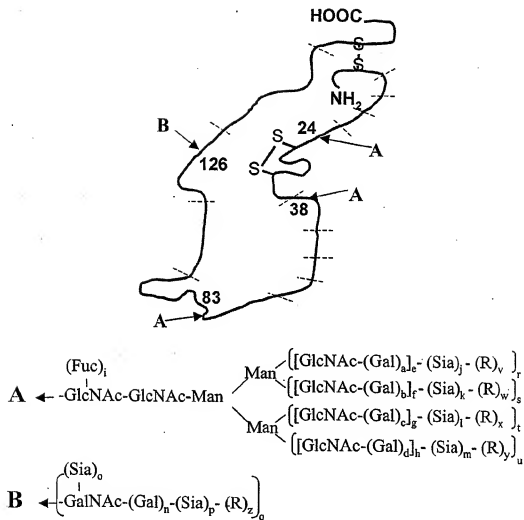
CHO, BHK, 293 cells, Vero expressed FSH.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
  2. ST3Gal1, desialylated chorionic gonadotrophin (CG) produced in CHO.
  3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0;  
v-y (independently selected) = 0 or 1;  
R = linker-CG.

FIG. 34J

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = polymer.

FIG. 35A



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CHO, BHK, 293 cells, Vero expressed EPO  
 a-g, n, q = 1; h = 1 to 3;  
 j-m, i, o, p (independently selected) = 0 or 1;  
 r-u (independently selected) = 0 to 1; v-z = 0

- ↓
1. Sialidase
  2. CMP-SA-PEG, ST3Gal3

a-g, n, q = 1; h = 1 to 3;  
 i, o, p (independently selected) = 0 or 1;  
 r-u (independently selected) = 0 or 1;  
 j-m, v-y (independently selected) = 0 or 1;  
 R = PEG; z = 0.

FIG. 35B

Insect cell expressed EPO  
 a-d, f, h, j-q, s, u, v-z = 0;  
 e, g, i, r, t (independently selected) = 0 or 1.

- ↓
1. GNT's 1&2, UDP-GlcNAc
  2. Galactosyltransferase, UDP-Gal
  2. CMP-SA-PEG, ST3Gal3

b, d, f, h, k, m-q, s, u, w, y, z = 0;  
 a, c, e, g, i, r, t (independently selected) = 0 or 1;  
 j, l, v, x (independently selected) = 0 or 1;  
 R = PEG.

FIG. 35C

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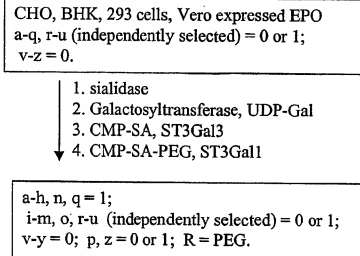


FIG. 35D

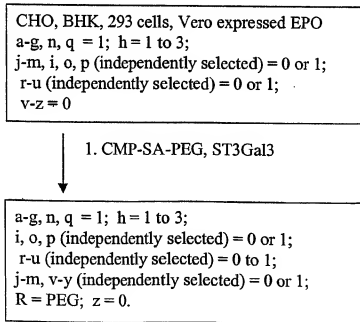


FIG. 35E

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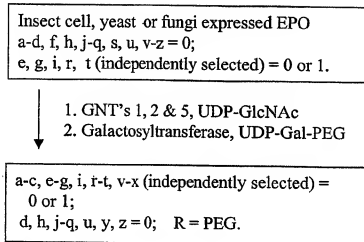


FIG. 35F

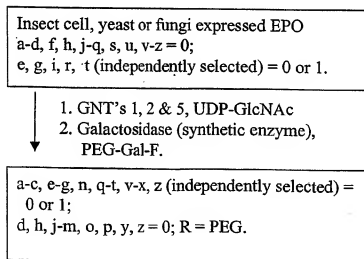


FIG. 35G

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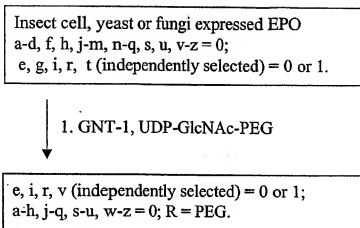


FIG. 35H

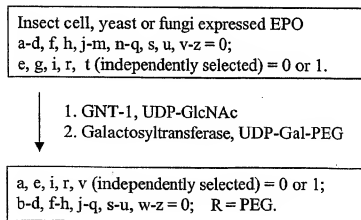


FIG. 35I

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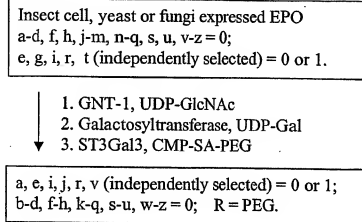


FIG. 35J

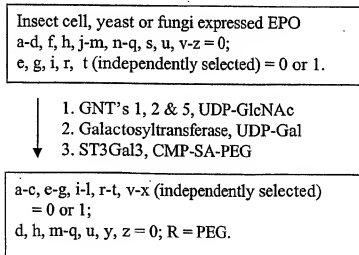


FIG. 35K

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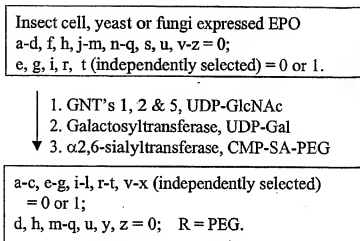


FIG. 35L

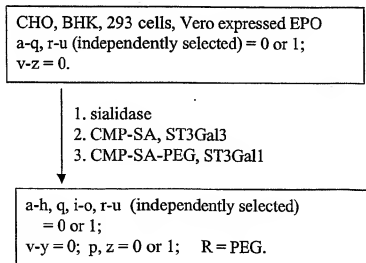


FIG. 35M

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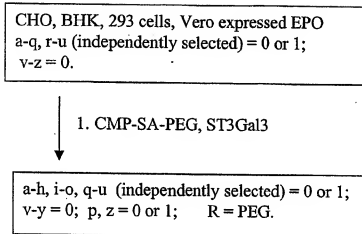


FIG. 35N

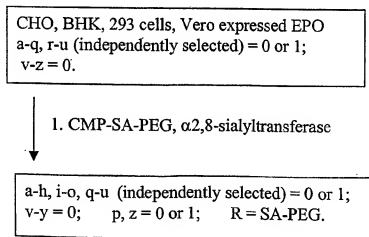


FIG. 35O

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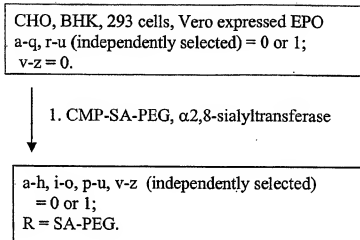


FIG. 35P

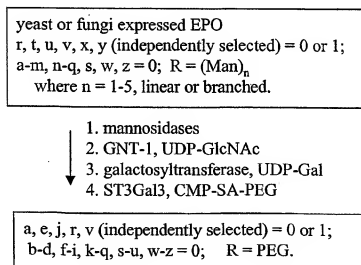


FIG. 35Q



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yeast or fungi expressed EPO  
 r, t, u, v, x, y (independently selected) = 0 or 1;  
 a-m, n-q, s, w, z = 0;  $R = (\text{Man})_n$   
 where n = 1-5, linear or branched.

- ↓
1. mannosidases
  2. GNT-1, UDP-GlcNAc-PEG

c, r, v (independently selected) = 0 or 1;  
 a-h, i-q, s-u, w-z = 0;  $R = \text{PEG}$ .

FIG. 35R

yeast or fungi expressed EPO  
 r, t, u, v, x, y (independently selected) = 0 or 1;  
 a-m, n-q, s, w, z = 0;  $R = (\text{Man})_n$   
 where n = 1-5, linear or branched.

- ↓
1. mannosidase-I
  2. GNT-1, UDP-GlcNAc
  3. galactosyltransferase, UDP-Gal
  4. ST3Gal3, CMP-SA-PEG

a, c, j, r, t-u, v, x, y (independently selected)  
 = 0 or 1;  
 b-d, f-i, k-q, s, w, z = 0;  
 $(R)_v = \text{PEG}$ ;  $(R)_x$  and  $(R)_y = \text{Man}$ .

FIG. 35S



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yeast or fungi expressed EPO  
 r, t, u, v, x, y (independently selected) = 0 or 1;  
 cc, a-m, n-q, s, w, z = 0;  
 aa, bb = 1;  
 $R = (\text{Man})_n$  where  $n = 1-100$ , linear or branched.

- ↓  
 1. endo-H  
 ↓  
 2. galactosyltransferase, UDP-Gal-PEG

i (independently selected) = 0 or 1;  
 aa, bb, cc, a-h, j-z = 0;  $R'' = \text{Gal-PEG}$ .

FIG. 35U

yeast or fungi expressed EPO  
 r, t, u, v, x, y (independently selected) = 0 or 1;  
 cc, a-m, n-q, s, w, z = 0; aa, bb = 1;  
 $R = (\text{Man})_n$  where  $n = 1-100$ , linear or branched.

- ↓  
 1. endo-H  
 ↓  
 2. galactosyltransferase, UDP-Gal  
 ↓  
 3. ST3Gal3, CMP-SA-PEG

i (independently selected) = 0 or 1;  
 aa, bb, cc, a-h, j-z = 0;  $R'' = \text{Gal-SA-PEG}$ .

FIG. 35V

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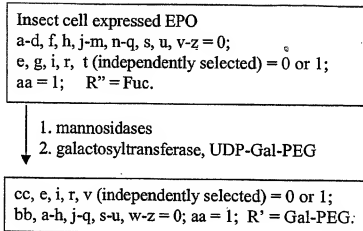


FIG. 35W



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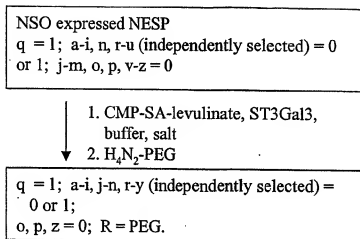


FIG. 35Y

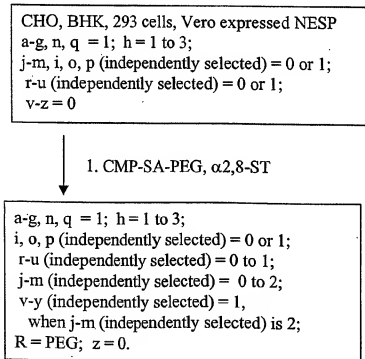


FIG. 35Z

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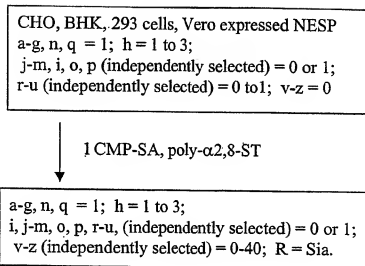
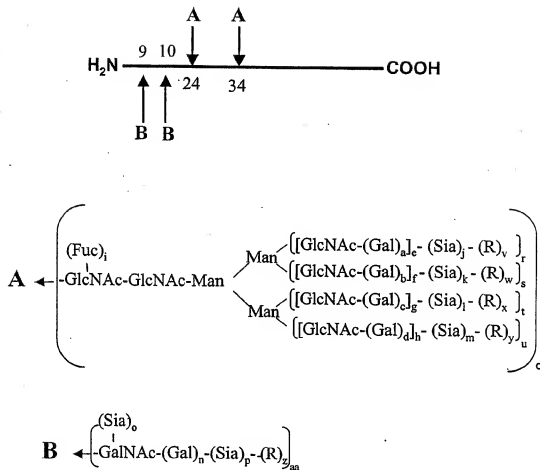


FIG. 35AA

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a-d, i, n-u, aa (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer, glycoconjugate.

FIG. 36A



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CHO, BHK, 293 cells, Vero expressed GM-CSF.  
a-d, i-m, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3

a-d, i-m, q-u, aa (independently selected) = 0 or 1;  
o, p, z = 0; n, e-h = 1;  
v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = PEG.

FIG. 36B

CHO, BHK, 293 cells, Vero expressed GM-CSF.  
a-d, i-m, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (1.2 mol eq),  
ST3Gal3
  3. CMP-SA (16 mol eq), ST3Gal3 &  
ST3Gal1

a-d, i-m, p-u, aa (independently selected) = 0 or 1;  
o, z = 0; n, e-h = 1;  
v-y (independently selected) = 0 or 1; R = PEG.

FIG. 36C

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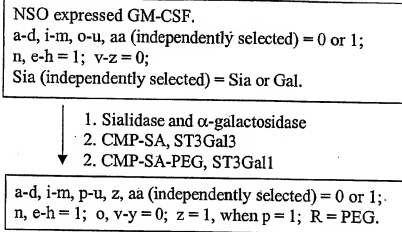


FIG. 36D

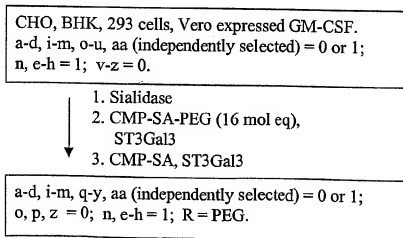


FIG. 36E

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CHO, BHK, 293 cells, Vero expressed GM-CSF.  
a-d, i-m, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; v-z = 0.



1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt
2. H<sub>4</sub>N<sub>2</sub>-PEG

a-d, i-m, o-y, aa (independently selected) = 0 or 1;  
z = 0; n, e-h = 1; R = PEG.

FIG. 36F

CHO, BHK, 293 cells, Vero expressed GMCSF.  
a-d, i-m, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; v-z = 0.

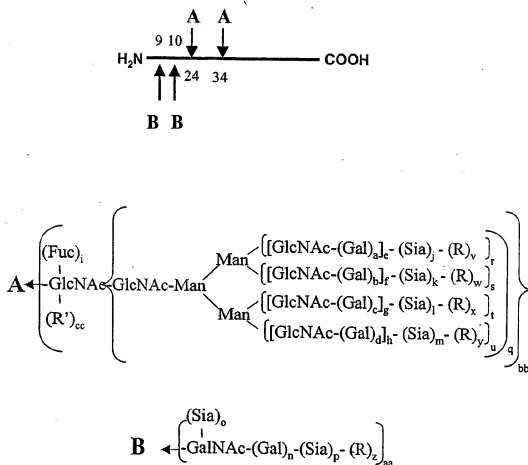


1. CMP-SA,  $\alpha$ 2,8-ST

a-d, i, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; j-m (independently selected) = 0-20;  
v-z (independently selected) = 0.

FIG. 36G

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a-d, i, n-u, aa, bb, cc (independently selected) = 0 or 1.

c-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 36H

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Insect cell expressed GM-CSF.

a-d, f, h, j-m, o, p, s, u, v-z = 0;

c, g, i, n, q, r, t, aa (independently selected) = 0 or 1.

1. GNT's 1,2,4,5, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal-PEG

a-i, n, q-u (independently selected) = 0 or 1;

j-m = 0; v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 36I

Yeast expressed GM-CSF.

a-p, z, cc = 0;

q-y, aa (independently selected) = 0 to 1;

bb = 1; R (branched or linear) = Man, oligomannose;

GalNAc = Man.

1. Endoglycanase
2. mannosidase (if aa = 1).
3. Galactosyltransferase, UDP-Gal-PEG

a-p, r-z, aa, bb = 0;


q, cc (independently selected) = 0 or 1;

R' = -Gal-PEG.

FIG. 36J

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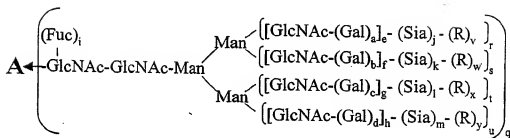
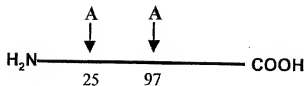
CHO, BHK, 293 cells, Vero expressed GM-CSF.  
a--m, o-u, aa, bb (independently selected) = 0 or 1;  
n, v-z, cc = 0.

- 
1. sialidase
  2. CMP-SA, ST3Gal3
  2. CMP-SA-linker-SA-CMP, ST3Gal1
  3. ST3Gal3, transferrin

a--m, p-u, z, aa (independently selected) = 0 or 1;  
o, v-y, cc = 0; bb, n = 1; R = transferrin.

FIG. 36K

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 37A

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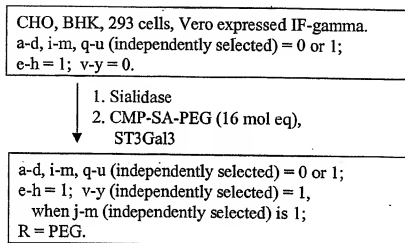


FIG. 37B

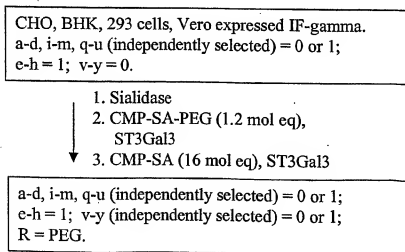


FIG. 37C



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NSO expressed Interferon gamma.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0;  
Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and  $\alpha$ -galactosidase
  2.  $\alpha$ -Galactosyltransferase, UDP-Gal
  - ▼ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = PEG.

FIG. 37D

CHO, BHK, 293 cells, Vero expressed  
Interferon gamma.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3
  - ▼ 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 37E

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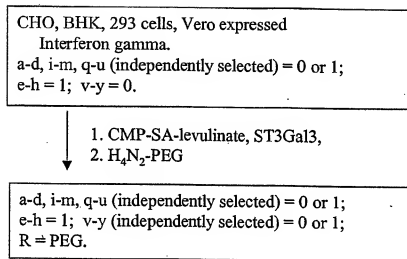


FIG. 37F

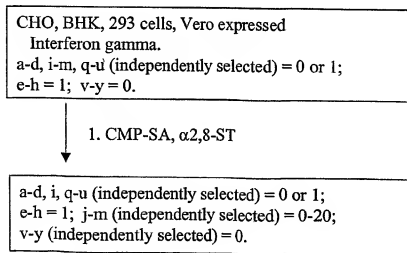


FIG. 37G



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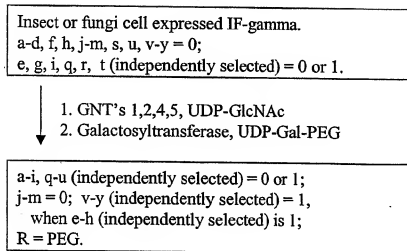


FIG. 37I

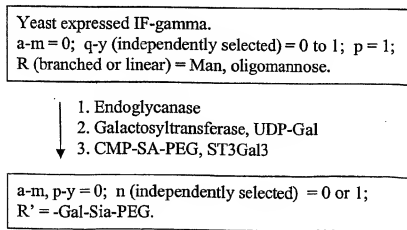


FIG. 37J

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CHO, BHK, 293 cells, Vero expressed IF-gamma.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP, ST3Gal3
  2. Galactosyltransferase, transferrin treated with endoglycanase.

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0;  
v-y (independently selected) = 0 or 1;  
R = linker-transferrin.

FIG. 37K

CHO, BHK, 293 cells, Vero expressed  
Interferon gamma.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h, p = 1; n, v-y = 0.

- ↓
1. CMP-SA-PEG,  
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h, p = 1;  
n, v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 37L

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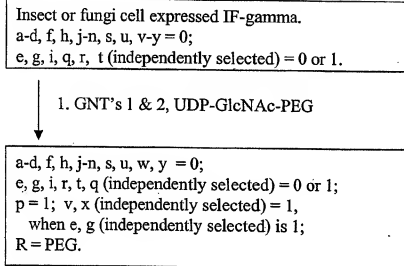


FIG. 37M

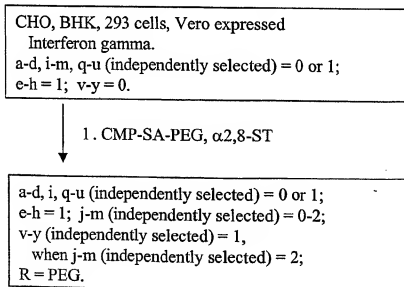


FIG. 37N



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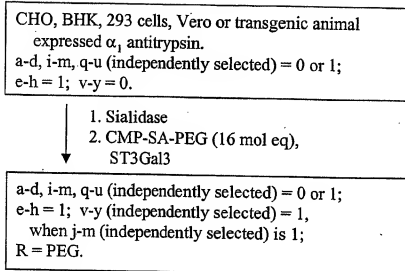


FIG. 38B

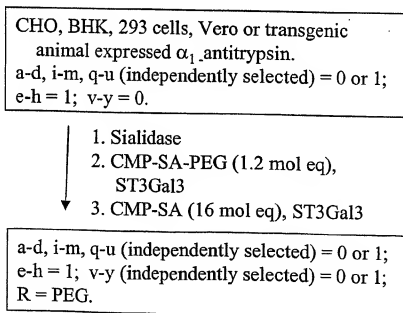


FIG. 38C



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CHO, BHK, 293 cells, Vero or transgenic animal  
expressed alpha-1 antitrypsin.

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3
  3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 38D

CHO, BHK, 293 cells, Vero or transgenic animal  
expressed  $\alpha_1$ -antitrypsin.

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt
  2.  $H_4N_2$ -PEG

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 38E

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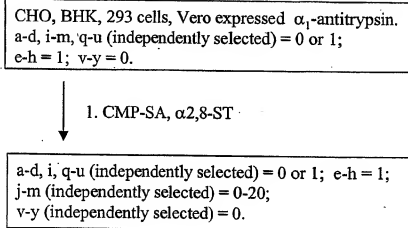
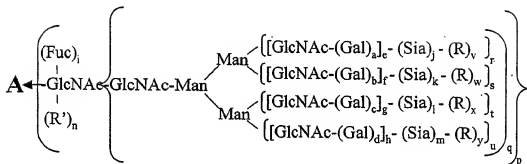
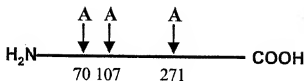


FIG. 38F

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 38G

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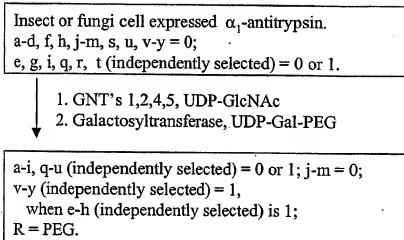


FIG. 38H

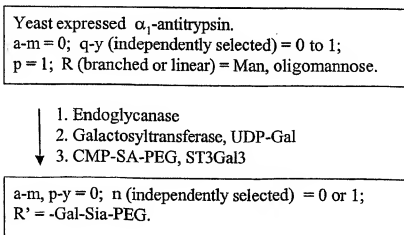


FIG. 38I

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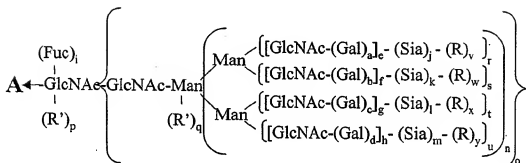
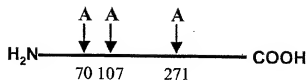
CHO, BHK, 293 cells, Vero expressed  $\alpha_1$ -antitrypsin.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,  
ST3Gal3
  2. Galactosyltransferase, transferrin treated  
with endoglycanase

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0;  
v-y (independently selected) = 0 or 1;  
R = linker-transferrin.

FIG. 38J

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer;

R', R'' (independently selected) = sugar, glycoconjugate.

FIG. 38K

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Yeast expressed alpha-1 antitrypsin.

a-h, i-m, p, q = 0;

R (independently selected) = mannose, oligomannose, polymannose;

r-u, v-y (independently selected) = 0 or 1; n, o = 1.

↓ 1. endoglycanase

▼ 2. Galactosyltransferase, UDP-Gal-PEG

a-h, i-o, q, r-u, v-y = 0; p = 1.

R'' = Gal-PEG.

FIG. 38L

Plant expressed alpha-1 antitrypsin.

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1;

n = 1; R' = xylose

↓ 1. hexosaminidase,

2. alpha mannosidase and xylosidase

▼ 3. GlcNAc transferase, UDP-GlcNAc-PEG

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, r, t (independently selected) = 0;

q = 1; R' = GlcNAc-PEG.

FIG. 38M

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CHO, BHK, 293 cells, Vero, transgenic animal  
expressed  $\alpha_1$  antitrypsin.  
a-h, i-o, r-u (independently selected) = 0 or 1;  
p, q, v-y = 0.

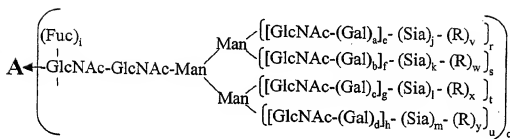
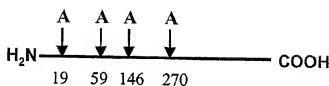
↓  
1. CMP-SA-PEG,  
ST3Gal3

a-h, i-o, r-u (independently selected) = 0 or 1;  
p, q = 0; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 38N



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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 39A

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CHO, BHK, 293 cells, Vero expressed Cerezyme  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (16 mol eq),  
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = PEG.

FIG. 39B

CHO, BHK, 293 cells, Vero expressed Cerezyme.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-M-6-P (1.2 mol eq),  
ST3Gal3
3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = mannose-6-phosphate

FIG. 39C

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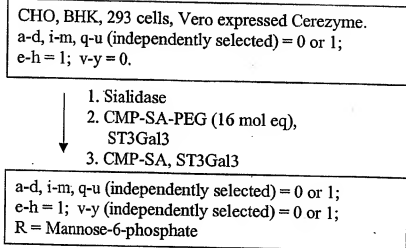


FIG. 39D

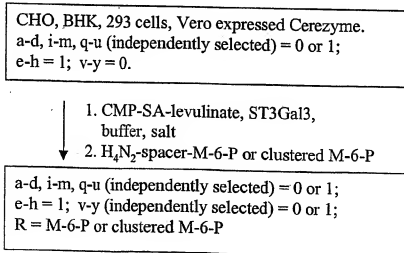


FIG. 39E

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CHO, BHK, 293 cells, Vero expressed Cerezyme.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

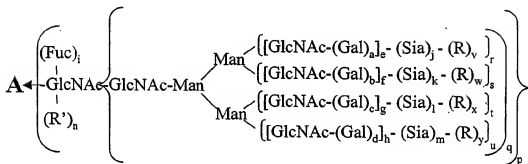
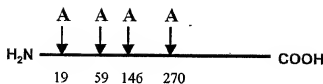


1. CMP-SA,  $\alpha$ 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;  
e-h = 1; j-m (independently selected) = 0-20;  
v-y (independently selected) = 0.

FIG. 39F

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 39G

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Insect cell expressed Cerezyme.

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;

j-m = 0;

v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 39H

Yeast expressed Cerezyme.

a-m = 0; q-y (independently selected) = 0 to 1;

p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3

a-m, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 39I

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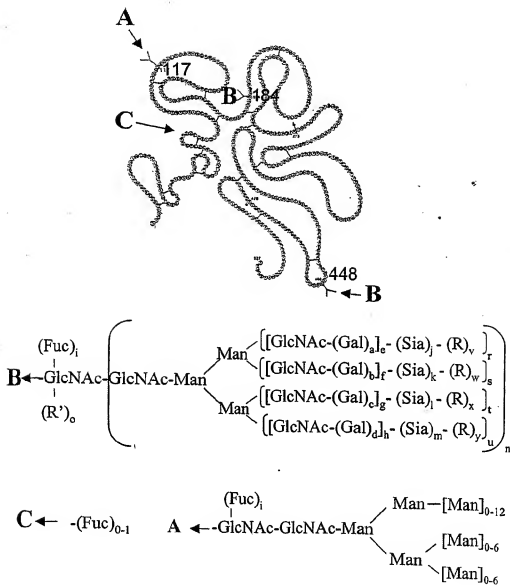
CHO, BHK, 293 cells, Vero expressed Cerezyme.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP,  
ST3Gal3
  2. ST3Gal3, desialylated transferrin.
  3. CMP-SA, ST3Gal3

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0; v-y (independently selected) = 0 or 1;  
R = linker-transferrin.

FIG. 39J

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer; R' = sugar, glycoconjugate.

FIG. 40A



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CHO, BHK, 293 cells, Vero expressed tPA  
 a-g, n = 1; h = 1 to 3;  
 j-m, i, (independently selected) = 0 or 1;  
 r-u (independently selected) = 0 to 1; o, v-y = 0.

1. Mannosidase(s), sialidase
2. GNT1,2 (4 and/or 5) UDP-GlcNAc
3. Gal transferase, UDP-Gal
- ▼ 4. CMP-SA-PEG, ST3Gal3

A = B; a-g, n = 1; h = 1 to 3;  
 i, r-u (independently selected) = 0 or 1;  
 o = 0; j-m, v-y (independently selected) = 0 or 1;  
 R = PEG

FIG. 40B

Insect or fungi cell expressed tPA  
 A = B; a-d, f, h, j-o, s, u, v-y = 0;  
 e, g, i, n, r, t (independently selected) = 0 or 1.

1. GNT's 1&2, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal
- ▼ 3. CMP-SA-PEG, ST3Gal3

A = B; b, d, f, h, k, m, o, s, u, w, y = 0;  
 a, c, e, g, i, r, t (independently selected) = 0 or 1;  
 n = 1; j, l, v, x (independently selected) = 0 or 1;  
 R = PEG.

FIG. 40C

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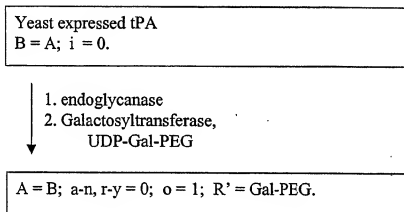


FIG. 40D

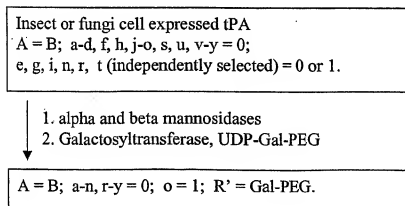


FIG. 40E

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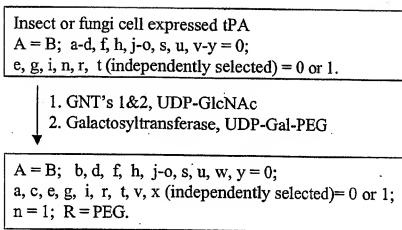


FIG. 40F

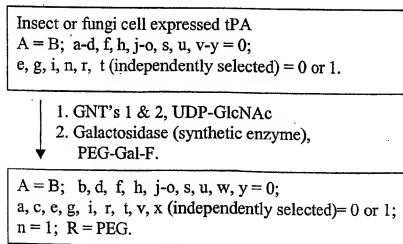
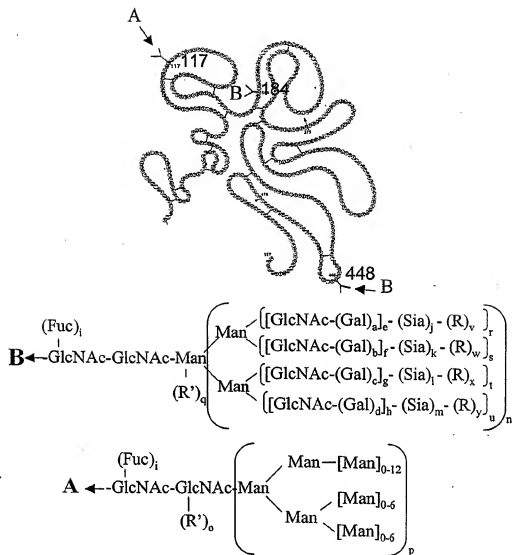


FIG. 40G

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer; R' = sugar, glycoconjugate.

FIG. 40H

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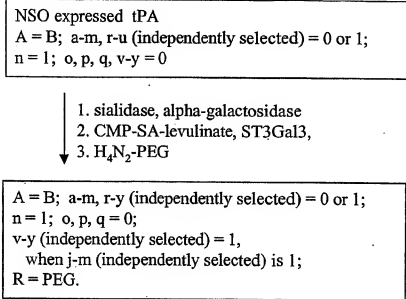


FIG. 40I

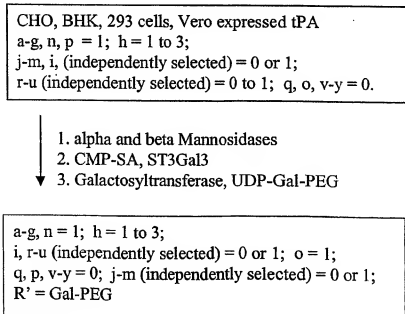


FIG. 40J

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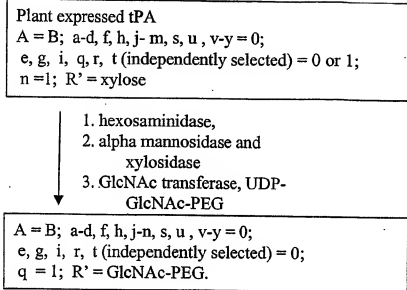


FIG. 40K



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CHO, BHK, 293 cells, Vero expressed TNK tPA  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (16 mol eq),  
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = PEG.

FIG. 40M

CHO, BHK, 293 cells, Vero expressed TNK tPA  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (1.2 mol eq),  
ST3Gal3
3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 40N



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NSO expressed TNK tPA

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and  $\alpha$ -galactosidase
  2. Galactosyltransferase, UDP-Gal
  3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

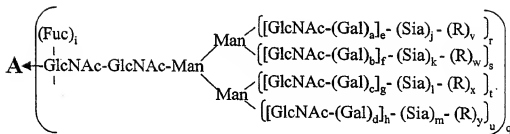
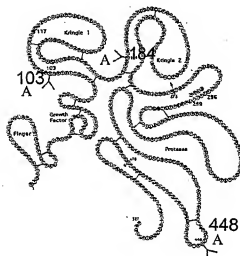
e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 400

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 40P

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CHO, BHK, 293 cells, Vero expressed TNK tPA  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3
  3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 40Q

CHO, BHK, 293 cells, Vero expressed TNK tPA  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt
  2. H<sub>4</sub>N<sub>2</sub>-PEG

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 40R

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CHO, BHK, 293 cells, Vero expressed TNK tPA  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

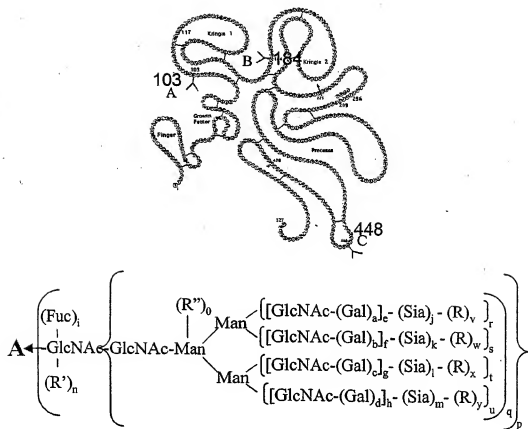


1. CMP-SA,  $\alpha$ 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;  
e-h = 1; j-m (independently selected) = 0-20;  
v-y (independently selected) = 0.

FIG. 40S

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a-d, i, n-y (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

R'' = glycosyl residue.

FIG. 40T

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Insect cell expressed TNK tPA

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;

j-m = 0; v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 40U

Yeast expressed TNK tPA

a-m = 0; q-y (independently selected) = 0 to 1; p = 1;

R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal-PEG

a-m, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-PEG.

FIG. 40V

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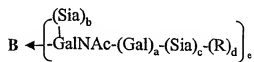
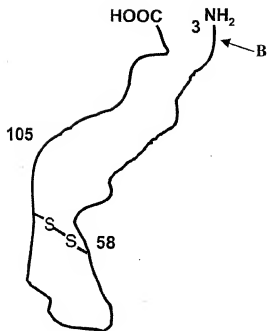
CHO, BHK, 293 cells, Vero expressed TNK tPA  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,  
ST3Gal3
  2. Galactosyltransferase, anti-TNF  
IG chimera produced in CHO.

a-m, r-u (independently selected) = 0 or 1; p, q = 1;  
n = 0; v-y (independently selected) = 0 or 1;  
R = linker-anti-TNF IG chimera protein.

FIG. 40W

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a-c, e (independently selected) = 0 or 1;  
 d = 0;  
 R = modifying group, mannose, oligo-  
 mannose.

FIG. 41A



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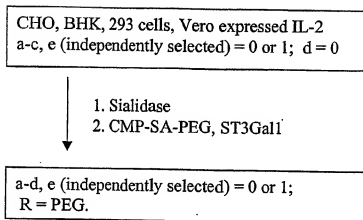


FIG. 41B

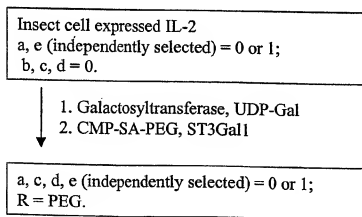


FIG. 41C

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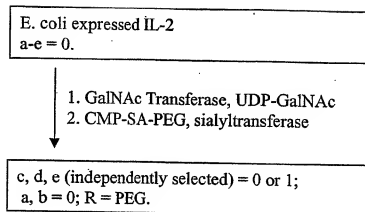


FIG. 41D

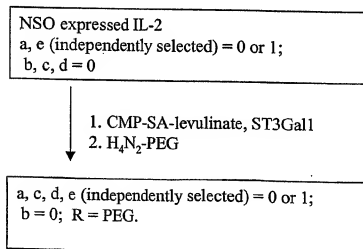


FIG. 41E

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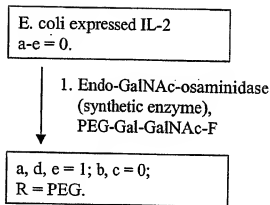


FIG. 41F

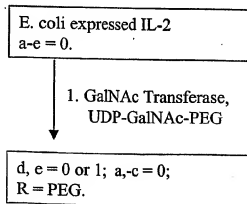
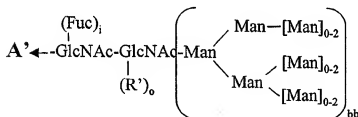
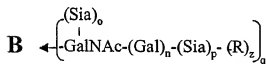
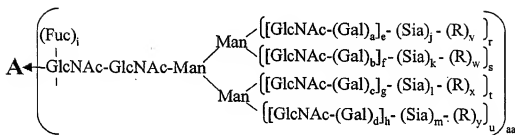


FIG. 41G

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2 peptides  
 A and A' - N-linked sites  
 B - O-linked sites



Alternate structure  
 for some N-linked  
 structures of A.

a-d, i, n-u (independently selected) = 0 or 1.  
 aa, bb (independently selected) = 0 or 1.  
 e-h (independently selected) = 0 to 6.  
 j-m (independently selected) = 0 to 20.  
 v-z = 0; R = polymer, glycoconjugate.

FIG. 42A

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CHO, BHK, 293s cells, Vero, MDCK, HEKC expressed  
Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected) = 0 or 1;

v-z = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG, ST3Gal3

e-h = 1 to 4;

aa, bb, a-d, i, n, q-u (independently selected) = 0 or 1;

o, p, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42B

CHO, BHK, 293S cells, Vero, MDCK, 293S, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected) = 0 or 1;

v-z = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG, ST3Gal3
  3. ST3Gal1, CMP-SA

e-h = 1 to 4;

aa, bb, a-d, i, n, p-u (independently selected) = 0 or 1;

o, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42C

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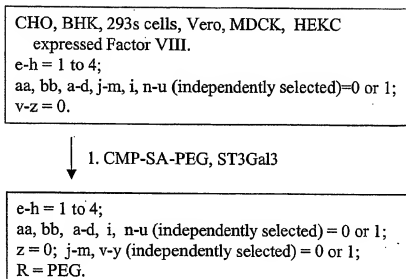


FIG. 42D

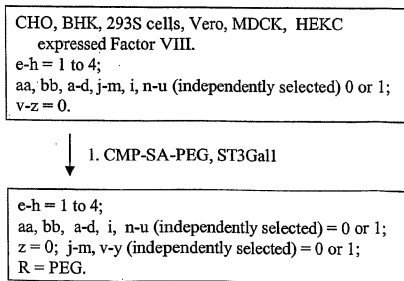


FIG. 42E

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CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected)=0 or 1;  
v-z = 0.



1. CMP-SA-PEG,  $\alpha$ 2,8-ST

e-h = 1 to 4;

aa, bb, a-d, i, n-y (independently selected) = 0 or 1;

z = 0; j-m (independently selected) = 0 to 2;

v-y (independently selected) = 1,

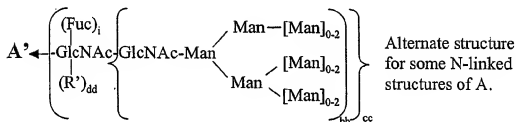
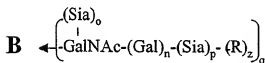
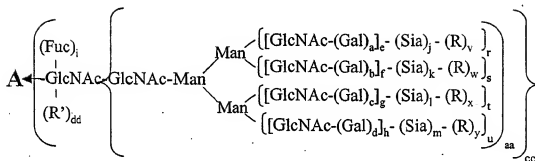
when j-m (independently selected) is 2;

R = PEG.

FIG. 42F

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2 peptides

**A or A'** - N-linked sites**B** - O-linked sites

a-d, i, n-u, (independently selected) = 0 or 1.

aa, bb, cc, dd (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 42G



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CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
  2. H<sub>4</sub>N<sub>2</sub>-PEG

e-h = 1 to 4;

aa, bb, cc, a-d, i, n-u (independently selected) = 0 or 1;

dd, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42H

CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓
1. endo-H
  2. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, bb, dd, a-d, i, j-u (independently selected) = 0 or 1;

cc, v-z = 0; R' = -Gal-PEG.

FIG. 42I

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CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;  
dd, v-z = 0.

- ↓
1. ST3Gal3, CMP-SA
  2. endo-H
  3. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, bb, dd, a-d, i, j-u (independently selected) = 0 or 1;  
cc, v-z = 0; R' = -Gal-PEG.

FIG. 42J

CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;  
dd, v-z = 0.

- ↓
1. mannosidases
  2. GNT 1 & 2, UDP-GlcNAc
  3. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, a-d, i, j-y (independently selected) = 0 or 1;  
bb, cc, dd, z = 0; R = PEG.

FIG. 42K

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CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;  
dd, v-z = 0.

- ↓
1. mannosidases
  2. GNT-1, 2, 4 & 5; UDP-GlcNAc
  3. galactosyltransferase, UDP-Gal
  4. ST3Gal3, CMP-SA

e-h = 1 to 4;

aa, bb, cc, a-d, i, j-q (independently selected) = 0 or 1;  
dd, v-z = 0.

FIG. 42L

CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;  
dd, v-z = 0.

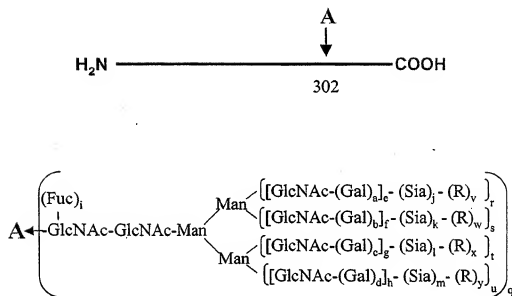
- ↓
1. mannosidases
  2. GNT-1, UDP-GlcNAc-PEG

e-h = 0 to 4;

aa, a-d, i, j-y (independently selected) = 0 or 1;  
bb, cc, dd, z = 0.

FIG. 42M

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 43A

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CHO, BHK, 293 cells, Vero expressed Urokinase.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (16 mol eq),  
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = PEG.

FIG. 43B

CHO, BHK, 293 cells, Vero expressed Urokinase.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (1.2 mol eq),  
ST3Gal3
3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 43C

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CHO, BHK, 293 cells, Vero expressed Urokinase.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3
  3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 43D

CHO, BHK, 293 cells, Vero expressed Urokinase.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt
  2. H<sub>4</sub>N<sub>2</sub>-PEG

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 43E

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CHO, BHK, 293 cells, Vero expressed Urokinase.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

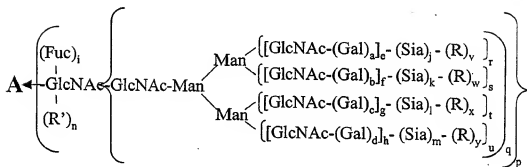
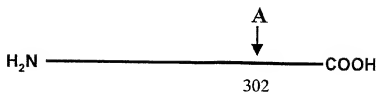


1. CMP-SA,  $\alpha$ 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;  
e-h = 1;  
j-m (independently selected) = 0-20;  
v-y (independently selected) = 0.

FIG. 43F

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,  
glycoconjugate.

FIG. 43G



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Insect cell expressed Urokinase.

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;

j-n = 0; v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 43H

Yeast expressed Urokinase.

a-n = 0;

q-y (independently selected) = 0 to 1;

p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3

a-m, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 43I

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CHO, BHK, 293 cells, Vero expressed Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
  2. ST3Gal1, desialylated Urokinase produced in CHO.
  - ↓ 3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;

p = 1; n = 0;

v-y (independently selected) = 0 or 1;

R = linker-Urokinase.

FIG. 43J

Isolated Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0; n = 0;

Sia (independently selected) = Sia or SO<sub>4</sub>;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.

- ↓
1. sulfohydrolase
  2. CMP-SA-PEG, sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1;

n = 0; e-h = 1; Sia = Sia;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.

v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 43K

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Isolated Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; n = 0; v-y = 0;

Sia (independently selected) = Sia or SO<sub>4</sub>;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.

- ↓
1. sulfohydrolase, hexosaminidase
  2. UDP-Gal-PEG, galactosyltransferase

a-d, i, q-u (independently selected) = 0 or 1;

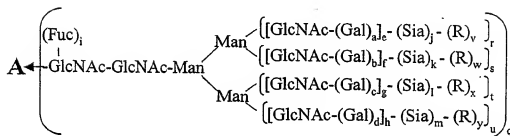
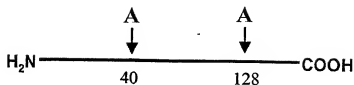
e-h = 1; j-n = 0; Gal (independently selected) = Gal;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc;

v-y (independently selected) = 0 or 1; R = PEG.

FIG. 43L

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer, glycoconjugate.

FIG. 44A

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CHO, BHK, 293 cells, Vero expressed DNase I.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1;  
v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = PEG.

FIG. 44B

CHO, BHK, 293 cells, Vero expressed DNase I.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (1.2 mol eq), ST3Gal3
  3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 44C

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CHO, BHK, 293 cells, Vero expressed DNase I.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (16 mol eq), ST3Gal3
3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 44D

CHO, BHK, 293 cells, Vero expressed DNase I.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.



1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt
2. H<sub>4</sub>N<sub>2</sub>-PEG

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 44E

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CHO, BHK, 293 cells, Vero expressed DNase I.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.



1. CMP-SA,  $\alpha$ 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;  
e-h = 1;  
j-m (independently selected) = 0-20;  
v-y (independently selected) = 0.

FIG. 44F





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Insect cell expressed DNase I.

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1; j-n = 0;

v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 44H

Yeast expressed DNase I.

a-n = 0;

q-y (independently selected) = 0 to 1;

p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase
2. Galactosyltransferase, UDP-Gal
3. CMP-SA-PEG, ST3Gal3

a-n, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 44I

198/498

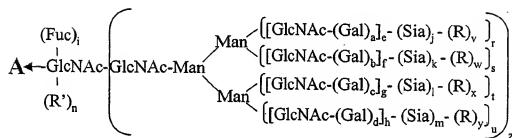
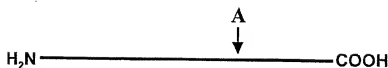
CHO, BHK, 293 cells, Vero expressed DNase I.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; n, v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
  2. ST3Gal1, desialylated alpha-1-Proteinase inhibitor.
  3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0;  
v-y (independently selected) = 0 or 1;  
R = linker- alpha-1-Proteinase inhibitor.

FIG. 44J

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,  
glycoconjugate.

FIG. 45A

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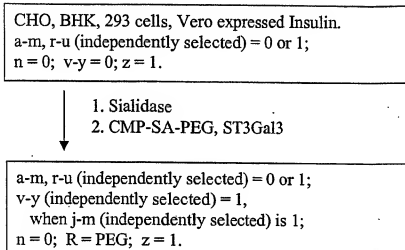


FIG. 45B

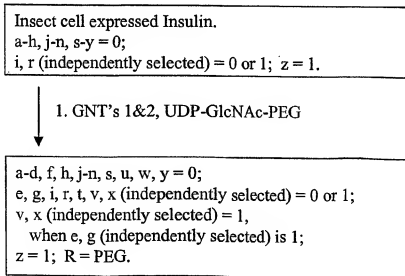


FIG. 45C

201/498

Yeast expressed Insulin.

a-n = 0; r-y (independently selected) = 0 to 1;

z = 1;

R (branched or linear) = Man, oligomannose or polysaccharide.



1. Endo-H

2. Galactosyltransferase, UDP-Gal-PEG

a-m, r-z = 0; n = 1; R' = -Gal-PEG.

FIG. 45D



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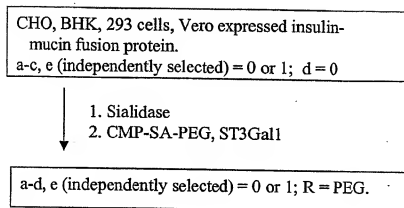


FIG. 45F

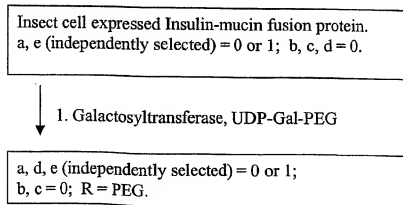


FIG. 45G

204/498

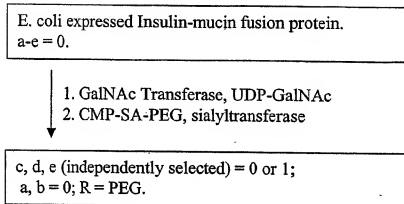
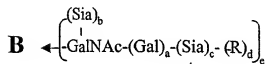
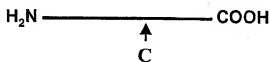
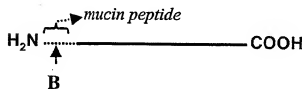
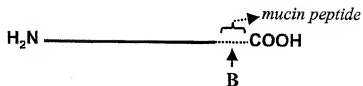


FIG. 45H



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a-c, e (independently selected) = 0 or 1;  
 d = 0; R = modifying group, mannose,  
 oligo-mannose.

FIG. 45I

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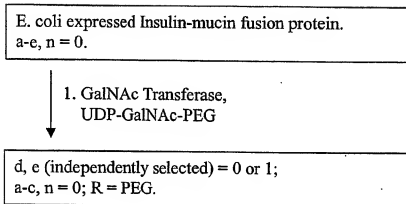


FIG. 45J

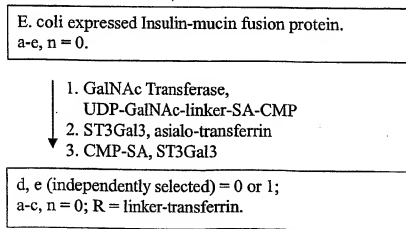


FIG. 45K

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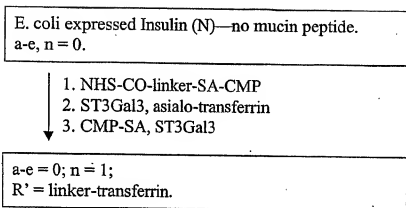
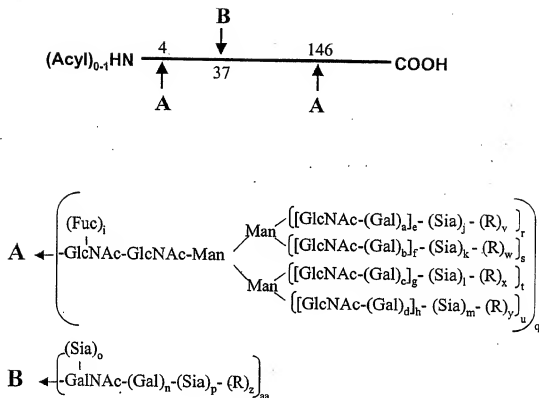


FIG. 45L

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a-d, i, n-u, aa (independently selected) = 0 or 1.  
 e-h (independently selected) = 0 to 6.  
 j-m (independently selected) = 0 to 100.  
 v-y = 0; R = polymer, glycoconjugate.

FIG. 46A

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CHO, BHK, 293 cells, Vero expressed M-antigen.  
a-d, i-m, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
  2. CMP-SA-linker-lipid-A,  
ST3Gal3

a-d, i-m, q-u, aa (independently selected) = 0 or 1;  
o, p, z = 0; n, e-h = 1;  
v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = linker-lipid-A.

FIG. 46B

CHO, BHK, 293 cells, Vero expressed M-antigen.  
a-d, i-m, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; v-z = 0.

- ↓
1. sialidase
  2. CMP-SA-linker-tetanus toxin, ST3Gal1
  3. CMP-SA, ST3Gal3

a-d, i-m, p-u, z, aa (independently selected) = 0 or 1;  
o, v-y = 0; n, e-h = 1; R = tetanus toxin.

FIG. 46C

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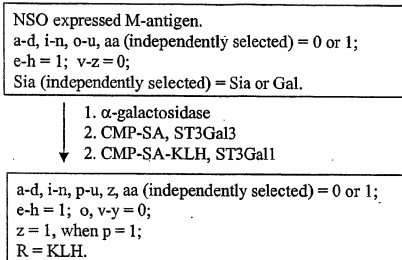


FIG. 46D

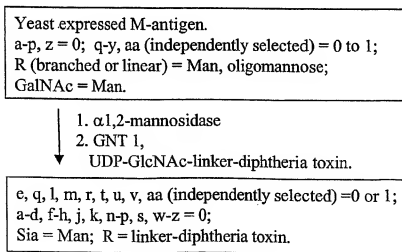


FIG. 46E

211/498

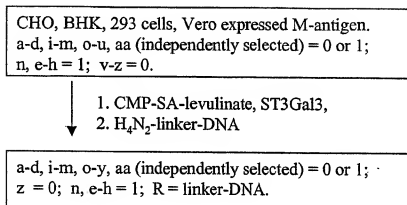


FIG. 46F

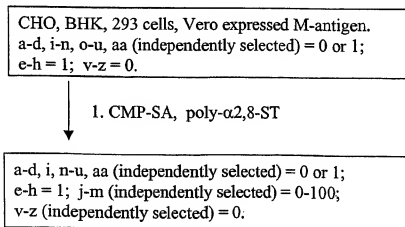
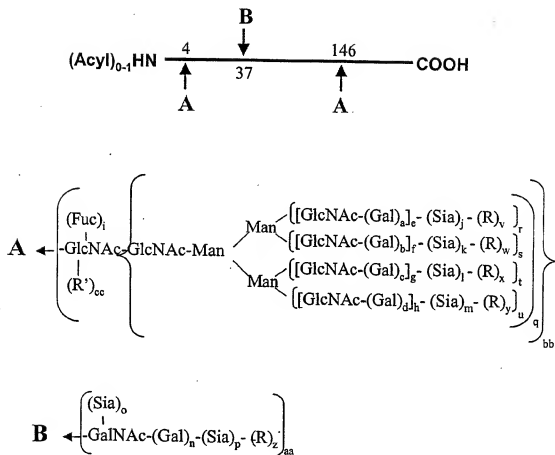


FIG. 46G

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a-d, i, n, q-u, aa, bb, (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-p (independently selected) = 0 to 100.

Cc, v-y = 0;

R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 46H



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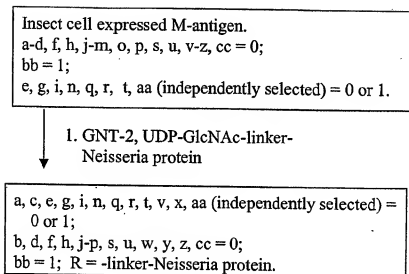


FIG. 46I

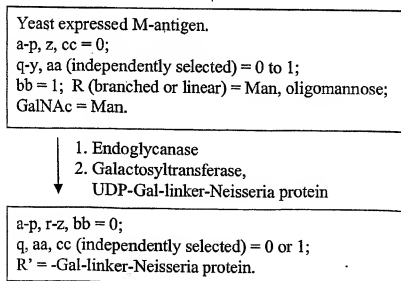


FIG. 46J

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Yeast expressed M-antigen.

a-p, z, cc = 0;

q-y, aa (independently selected) = 0 to 1; bb = 1;

R (branched or linear) = Man, oligomannose;

GalNAc = Man.

1. mannosidases

2. GNT 1 & 2, UDP-GlcNAc

3. UDP-Gal, Galactosyltransferase,

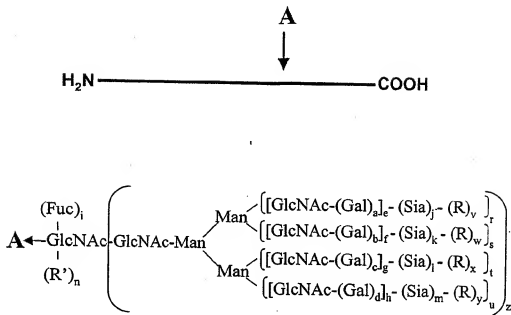
4. CMP-SA, sialyltransferase

a, c, e, g, j, l, q, r, t, aa (independently selected) = 0 or 1;

b, d, f, h, k, m-p, s, u-z, cc = 0; bb = 1.

FIG. 46K

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,  
glycoconjugate.

FIG. 47A

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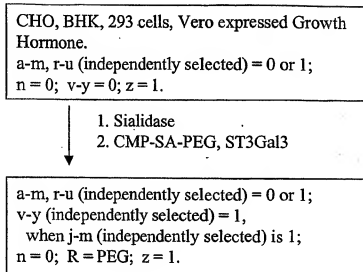


FIG. 47B

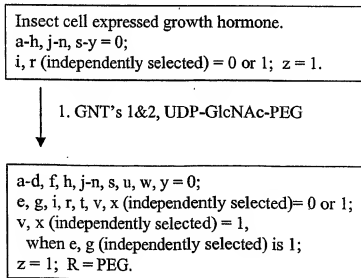


FIG. 47C

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Yeast expressed growth hormone.

a-n = 0; r-y (independently selected) = 0 to 1;

z = 1;

R (branched or linear) = Man, oligomannose or polysaccharide.

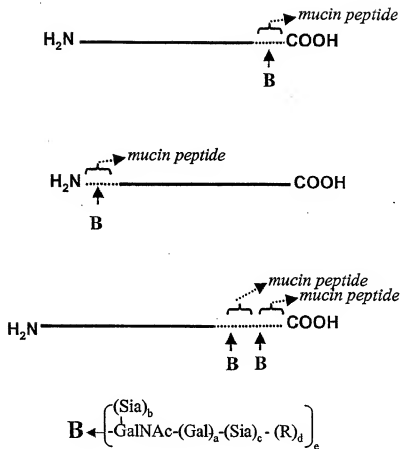
1. Endo-H

2. Galactosyltransferase, UDP-Gal-PEG

a-m, r-z = 0; n = 1; R' = -Gal-PEG.

FIG. 47D

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a-c, e (independently selected) = 0 or 1;

d = 0;

R = modifying group, mannose, oligo-mannose.

FIG. 47E

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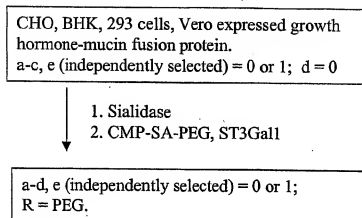


FIG. 47F

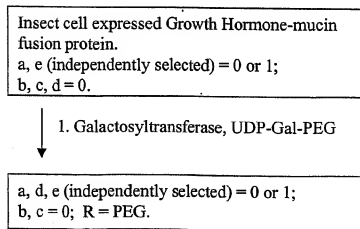


FIG. 47G

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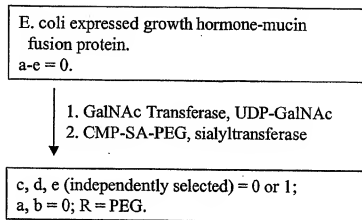


FIG. 47H

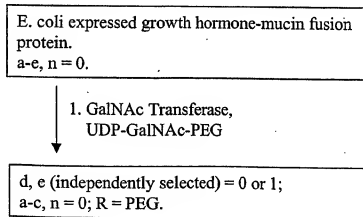


FIG. 47I



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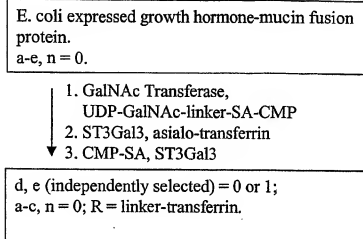


FIG. 47J

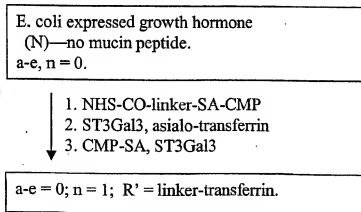
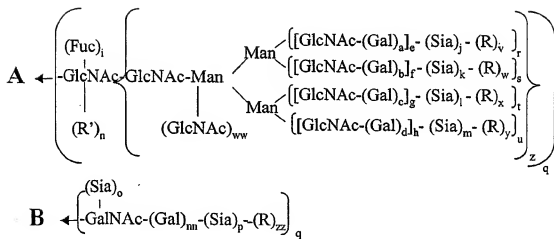
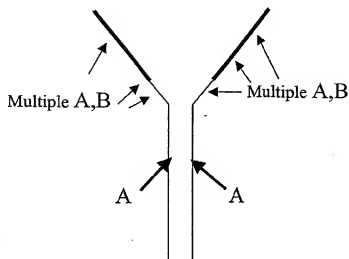


FIG. 47K

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a-d, i-m, q-u, w, z, nn, ww, zz (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

n, v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 48A

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CHO, BHK, 293 cells, Vero or transgenic animals  
expressed TNF Receptor IgG Fusion.

a-m, o-u, aa (independently selected) = 0 or 1;  
n = 1; v-z = 0.

- ↓
1. CMP-SA, ST3Gal1
  2. galactosyltransferase, UPD-Gal
  3. CMP-SA-PEG, ST3Gal3

a-m, o-u, v-y, aa (independently selected) = 0 or 1;  
n = 1; z = 0; R = PEG.

FIG. 48B

CHO, BHK, 293 cells, Vero expressed  
TNF Receptor IgG Fusion.

a-m, o-u, aa (independently selected) = 0 or 1;  
n = 1; v-z = 0.

- ↓
1. sialidase
  2. CMP-SA-PEG, ST3Gal1

a-i, p-u, z, aa (independently selected) = 0 or 1;  
n = 1; o, j-m, v-y = 0; R = PEG.

FIG. 48C

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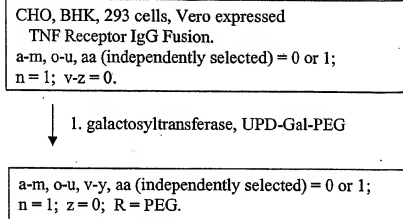


FIG. 48D

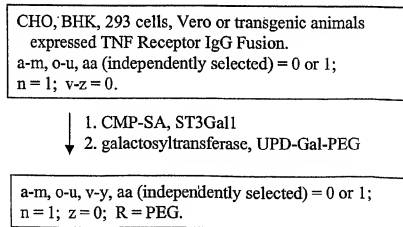


FIG. 48E

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CHO, BHK, 293 cells, Vero or transgenic animals  
expressed TNF Receptor IgG Fusion.

a-m, o-u, aa (independently selected) = 0 or 1;  
n = 1; v-z = 0.

- ↓  
1. CMP-SA-levulinate, ST3Gal1  
2. H<sub>4</sub>N<sub>2</sub>-PEG

a-m, o-u, v-y, aa (independently selected) = 0 or 1;  
n = 1; z = 0; R = PEG.

FIG. 48F

CHO, BHK, 293 cells, Vero expressed  
TNF Receptor IgG Fusion.

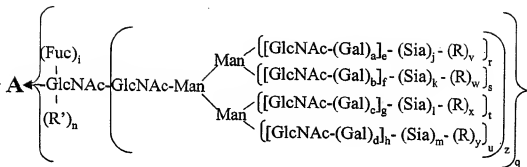
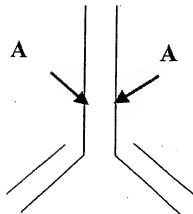
a-m, o-u, aa (independently selected) = 0 or 1;  
n = 1; v-z = 0.

- ↓  
1. CMP-SA-PEG,  $\alpha$ 2,8-ST

a-i, o, q-u, v-z, aa (independently selected) = 0 or 1;  
n = 1; j-m, p (independently selected) = 0 to 2;  
v-z (independently selected) = 1,  
when j-m, p (independently selected) is 2;  
R = PEG.

FIG. 48G

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a-d, i, l, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-k (independently selected) = 0 or 1.

M = 0 to 20.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 49A

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CHO, BHK, 293 cells, Vero expressed Herceptin.  
 a, c, i (independently selected) = 0 or 1;  
 e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;  
 q, z = 1.

- ↓  
 1. galactosyltransferase, UPD-Gal  
 2. CMP-SA-toxin, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;  
 e, g, r, t = 1; R = toxin;  
 f, h, k, m, n, s, u-y = 0; q, z = 1;  
 v-y (independently selected) = 51,  
 when j, l (independently selected) is 1.

FIG. 49B

CHO, BHK, 293 cells, Vero or fungal expressed Herceptin.  
 a, c, i (independently selected) = 0 or 1;  
 e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;  
 q, z = 1.

- ↓  
 1. galactosyltransferase,  
 UPD-Gal-Toxin

a, c, i (independently selected) = 0 or 1;  
 e, g, r, t = 1; f, h, j-m, n, s, u-y = 0;  
 q, z = 1; v-y (independently selected) = 1,  
 when a, c (independently selected) is 1;  
 R = toxin.

FIG. 49C

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Fungi expressed Herceptin.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

- ↓
1. Endo-H
  2. Galactosyltransferase, UDP-Gal
  - 3.. CMP-SA-radioisotope complex, ST3Gal3

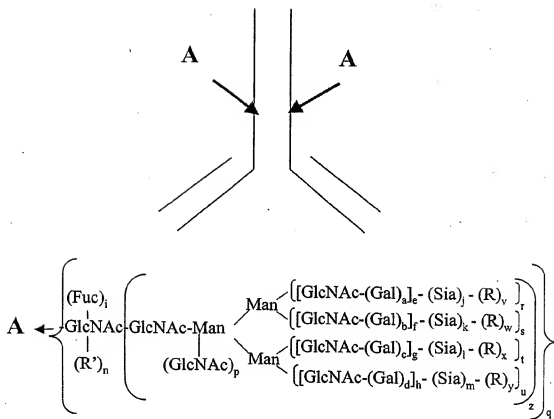
a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 49D



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a-d, i, p-u, (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 50A

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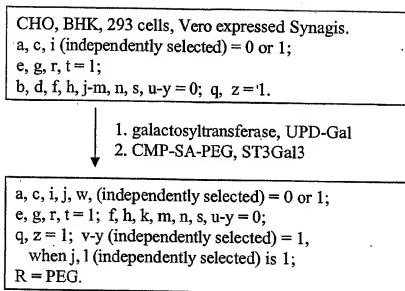


FIG. 50B

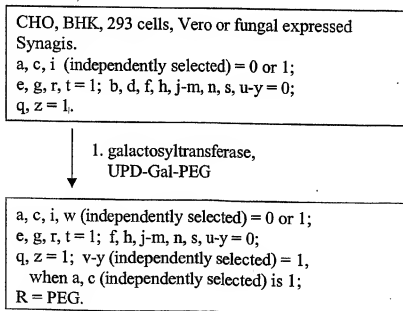


FIG. 50C

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Fungi expressed Synagis.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

1. Endo-H

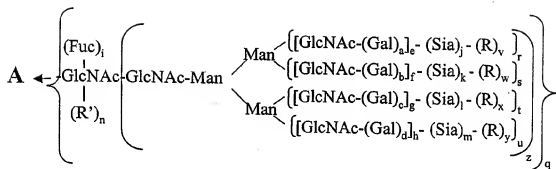
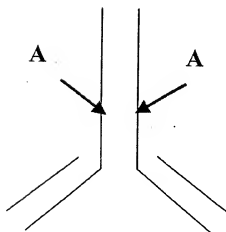
2. Galactosyltransferase, UDP-Gal

↓ 3.. CMP-SA-PEG, ST3Gal3

a-m, r-z= 0; q, n = 1; R' = -Gal-Sia-PEG.

FIG. 50D

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a-d, i, q-u, w (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 51A

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CHO, BHK, 293 cells, Vero expressed Remicade.

a, c, i (independently selected) = 0 or 1;  
e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;  
q, z = 1.



1. galactosyltransferase, UPD-Gal
2. CMP-SA-PEG, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;  
e, g, r, t = 1; f, h, k, m, n, s, u-y = 0;  
q, z = 1; v-y (independently selected) = 1,  
when j, l (independently selected) is 1;  
R = PEG.

FIG. 51B

CHO, BHK, 293 cells, Vero or fungal expressed Remicade.

a, c, i (independently selected) = 0 or 1;  
e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;  
q, z = 1.



1. galactosyltransferase,  
UPD-Gal-PEG

a, c, i (independently selected) = 0 or 1;  
e, g, r, t = 1; f, h, j-m, n, s, u-y = 0;  
q, z = 1; v-y (independently selected) = 1,  
when a, c (independently selected) is 1;  
R = PEG.

FIG. 51C

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Fungi expressed Remicade.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

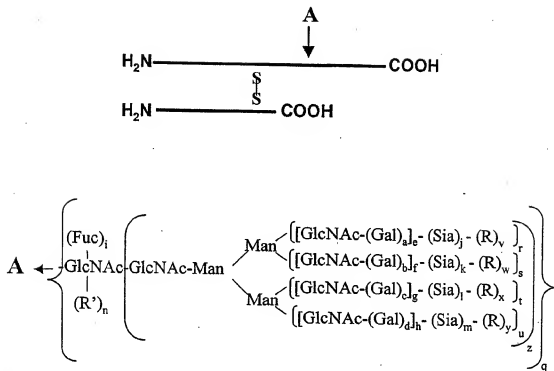
- ↓
1. Endo-H
  2. Galactosyltransferase, UDP-Gal
  - 3.. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 51D

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,  
glycoconjugate.

FIG. 52A

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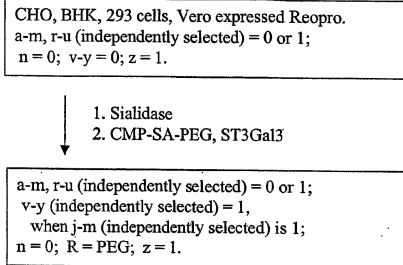


FIG. 52B

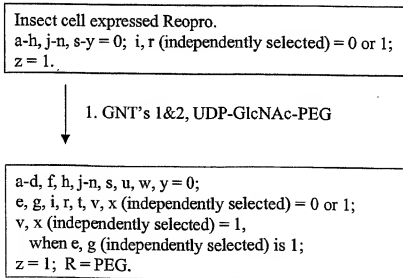


FIG. 52C



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Yeast expressed Reopro.

a-n = 0; r-y (independently selected) = 0 to 1;

z = 1;

R (branched or linear) = Man, oligomannose or polysaccharide.

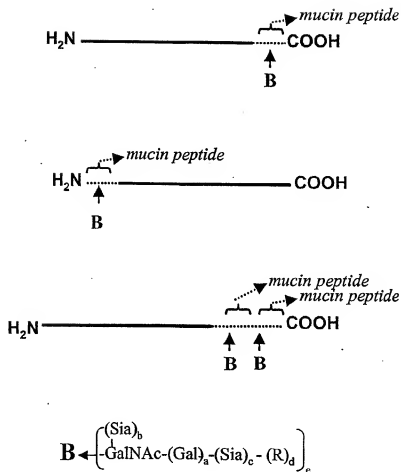
1. Endo-H

2. Galactosyltransferase, UDP-Gal-PEG

a-m, r-z= 0; n = 1; R' = -Gal-PEG.

FIG. 52D

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a-c, e (independently selected) = 0 or 1;  
 d = 0; R = polymer

FIG. 52E

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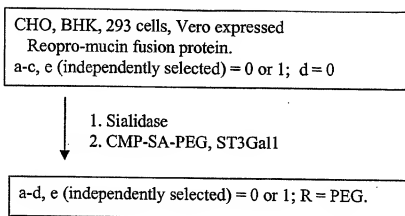


FIG. 52F

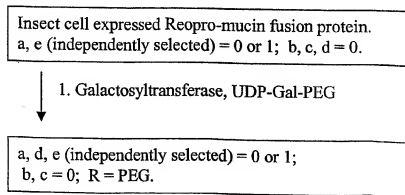


FIG. 52G

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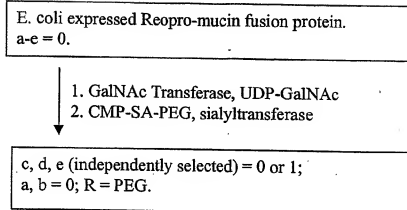
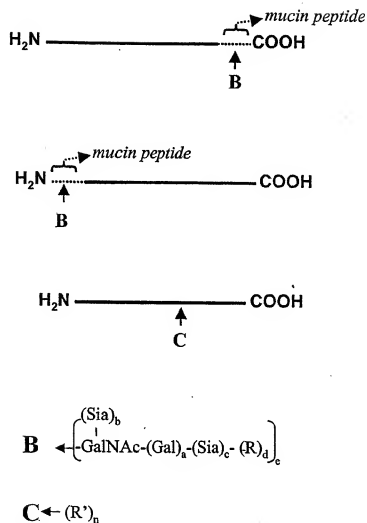


FIG. 52H

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a-c, e (independently selected) = 0 or 1;  
 d = 0; R = polymer, linker.

FIG. 52I

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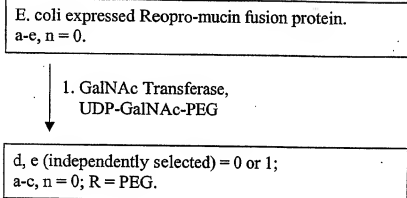


FIG. 52J

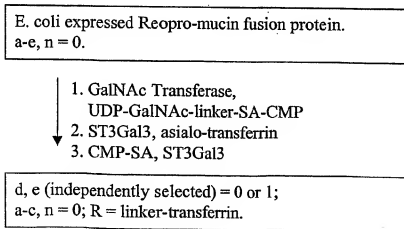


FIG. 52K

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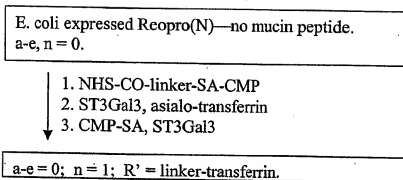
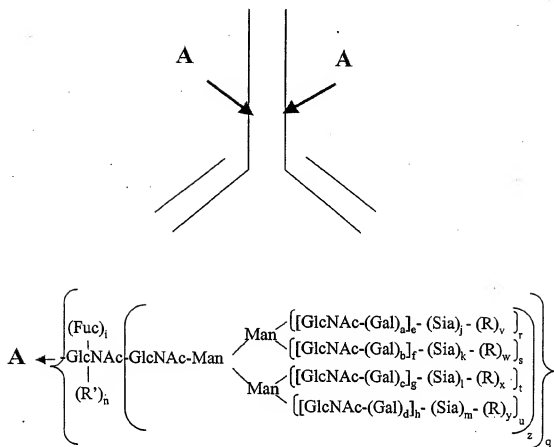


FIG. 52L

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1; R = polymer, toxin, radioisotope-complex, drug, glycoconjugate.

R' = H, sugar, glycoconjugate.

z

FIG. 53A



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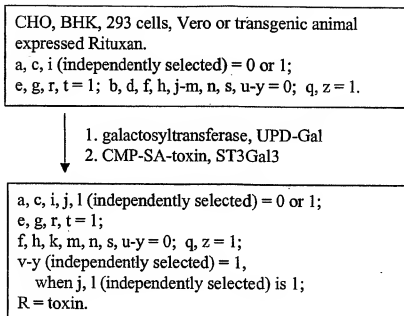


FIG. 53B

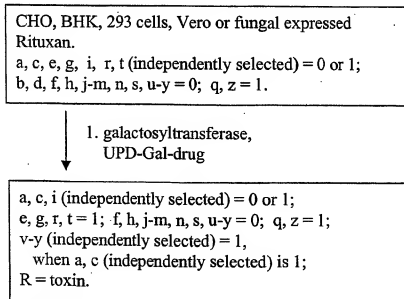


FIG. 53C

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Fungi expressed Rituxan.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

1. Endo-H

2. Galactosyltransferase, UDP-Gal

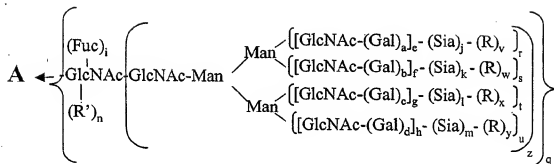
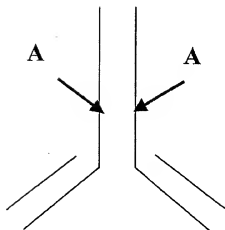
↓ 3. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 53D

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug,  
glycoconjugate, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 53E

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CHO, BHK, 293 cells, Vero or transgenic animal  
expressed Rituxan.

a, c, i (independently selected) = 0 or 1;  
e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;  
q, z = 1.



1. galactosyltransferase, UPD-Gal
2. CMP-SA-PEG, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;  
e, g, r, t = 1; f, h, k, m, n, s, u-y = 0;  
q, z = 1; v-y (independently selected) = 1,  
when j, l (independently selected) is 1;  
R = PEG.

FIG. 53F

Fungi, yeast or CHO expressed Rituxan.

e, g, i, r, t, v, x (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u, w, y = 0; q, z = 1;

R (independently selected) = mannose, oligomannose,  
polymannose.

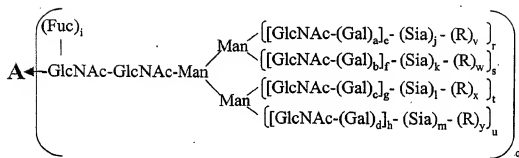
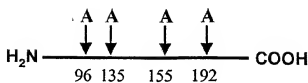


1. mannosidases (alpha and beta)
2. GNT-I,II, UDP-GlcNAc
3. Galactosyltransferase, UDP-Gal-radioisotope

a-m, r-z = 0; q, n = 1;  
R' = -Gal-radioisotope complex.

FIG. 53G

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = mannose, polymer.

FIG. 54A

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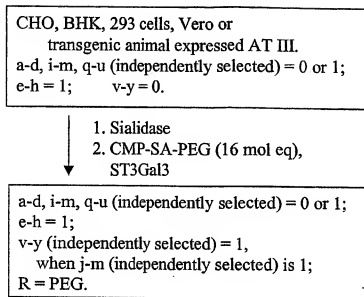


FIG. 54B

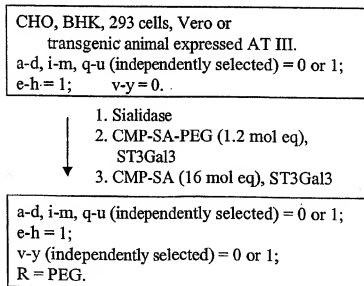


FIG. 54C

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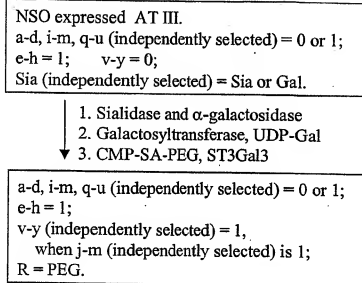


FIG. 54D

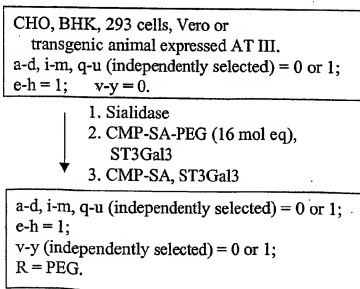


FIG. 54E

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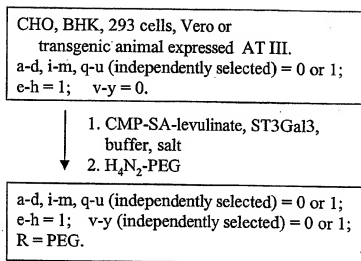


FIG. 54F

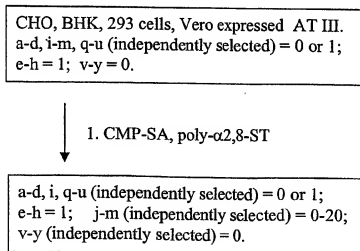
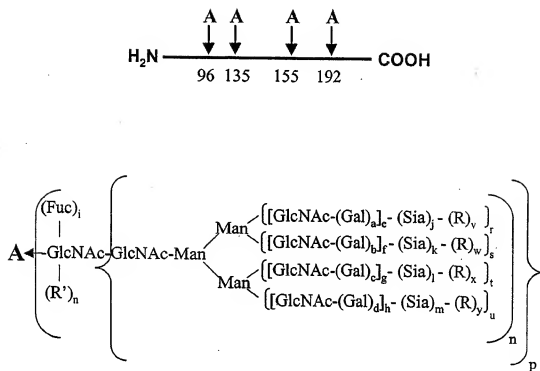


FIG. 54G



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a-d, i, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0 to 100.

R = polymer, linker, mannose.

R' = H, sugar, glycoconjugate.

FIG. 54H

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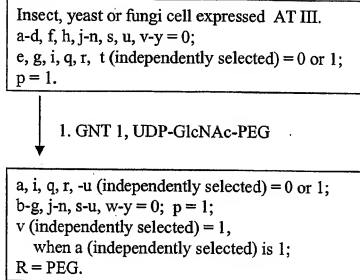


FIG. 54I

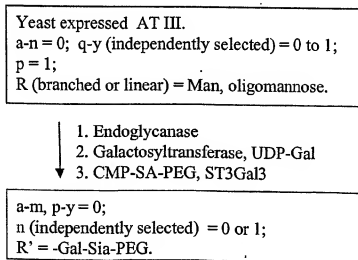


FIG. 54J

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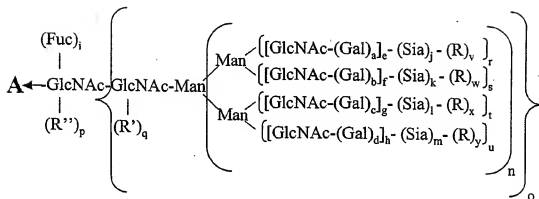
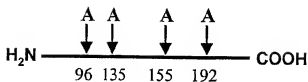
CHO, BHK, 293 cells, Vero expressed AT III.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,  
ST3Gal3
  2. Galactosyltransferase, transferrin  
treated with endoglycanase

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0;  
v-y (independently selected) = 0 or 1;  
R = linker-transferrin.

FIG. 54K

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer.

R', R'' (independently selected) = sugar, glycoconjugate.

FIG. 54L

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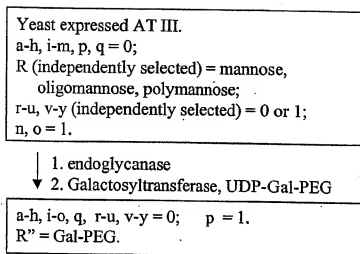


FIG. 54M

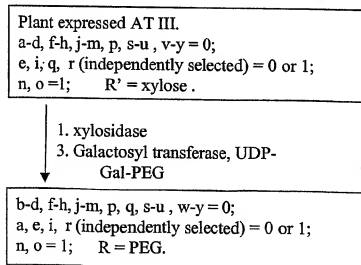


FIG. 54N

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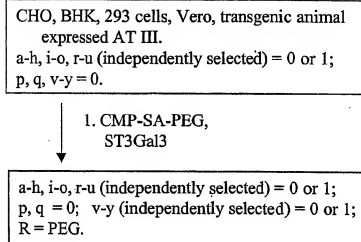
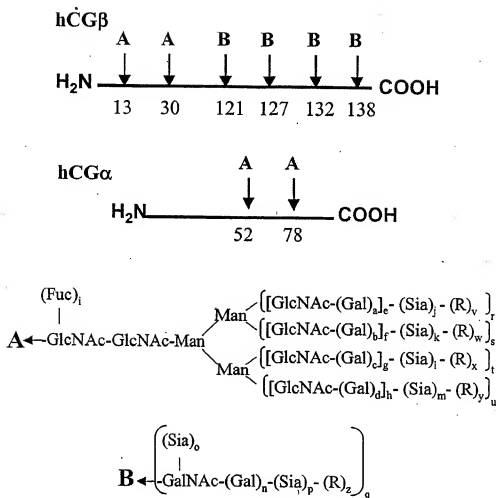


FIG. 54O

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0; R = polymer

FIG. 55A

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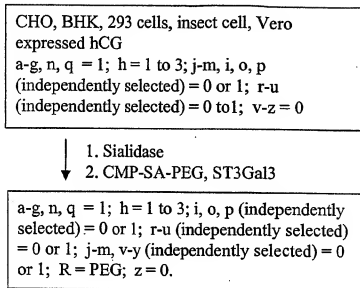


FIG. 55B

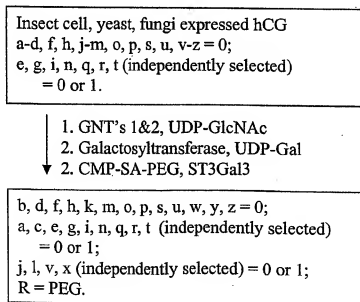


FIG. 55C



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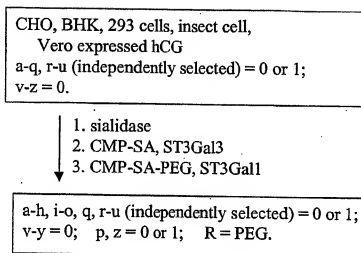


FIG. 55D

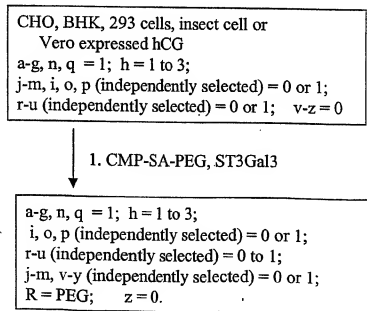


FIG. 55E

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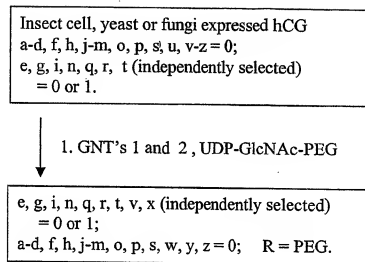


FIG. 55F

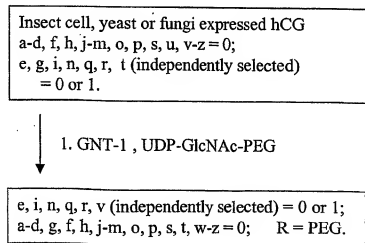


FIG. 55G

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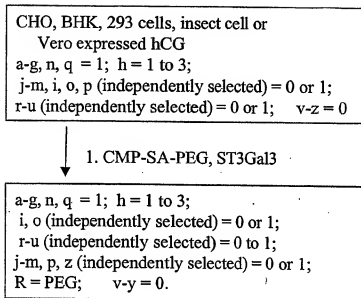


FIG. 55H

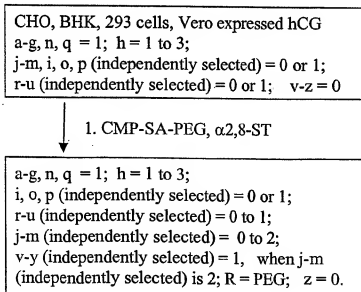


FIG. 55I

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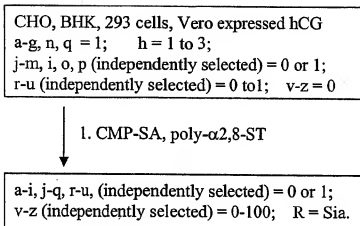
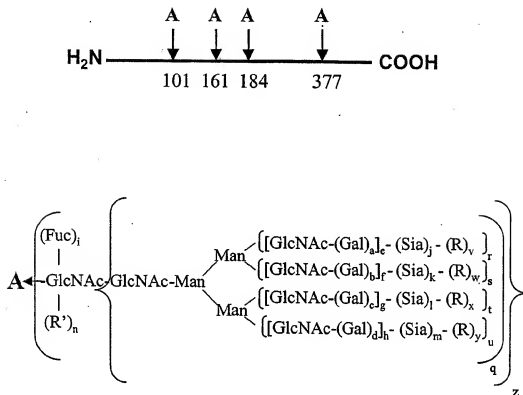


FIG. 55J

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a-d, i, n, q-u, z (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0 to 100;

R = mannose, mannose-6-phosphate and mannose, polymer.

FIG. 56A

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CHO, BHK, 293 cells, insect cells, Vero expressed and secreted alpha-galactosidase  
 a-h, i-m, q-u (independently selected) = 0 or 1;  
 z = 1; n, v-y = 0; and when a-n = 0, then r-u (independently selected) = 0 or 1; v-y (independently selected) = 0-100;  
 R = mannose or mannose with mannose-6-phosphate.

- ↓  
 1. Endo-H  
 2. Galactosyltransferase, UDP-Gal-PEG-transferrin

a-h, i-m, q-u (independently selected) = 0 or 1;  
 n, v-y = 0; z = 1; and when z = 0 and q = 1,  
 then n (independently selected) = 0 or 1;  
 R' = Gal-PEG-transferrin.

FIG. 56B

CHO, BHK, 293 cells, Insect cells,  
 Vero expressed and secreted alpha-galactosidase  
 a-h, i-m, q-u (independently selected) = 0 or 1; z = 1; n, v-y = 0; and when a-n = 0, then r-u (independently selected) = 0 or 1; v-y (independently selected) = 0-100;  
 R = mannose or mannose with mannose-6-phosphate.

- ↓  
 1. Sialidase  
 2. CMP-SA-linker-Mannose-6-phosphate  
 ST3Gal3

a-h, i-m, q-u, v-y (independently selected) = 0 or 1;  
 n = 0; z = 1; R = mannose-6-phosphate; and when a-n = 0, then r-u (independently selected) = 0 or 1;  
 v-y (independently selected) = 0-100;  
 R = mannose or mannose with mannose-6-phosphate.

FIG. 56C

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NSO expressed alpha-galactosidase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and  $\alpha$ -galactosidase
  2. Galactosyltransferase, UDP-Gal
  3. CMP-SA-linker-mannose-6-phosphate sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1; e-h = 1;  
v-y (independently selected) = 1, when j-m (independently selected) is 1; R = mannose-6 phosphate

FIG. 56D

CHO, BHK, 293 cells, Insect cells, Vero expressed and secreted alpha-galactosidase

a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;

n, v-y = 0; and when a-n = 0, then r-u (independently selected) = 0 or 1; v-y (independently selected) = 0-100;

R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Sialidase
  2. CMP-SA-PEG, sialyltransferase

a-h, i-m, q-u, v-y (independently selected) = 0 or 1; n = 0; z = 1; R = PEG; and when a-n = 0, then r-u (independently selected) = 0 or 1; v-y = 0-100; R = mannose or mannose with mannose-6-phosphate.

FIG. 56E

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CHO, BHK, 293 cells, Insect cells, Vero, yeast, fungi  
expressed alpha-galactosidase.  
a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;  
r-u (independently selected) = 0 or 1;  
j-m (independently selected) = 0-100;  
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. mannosyltransferase,  
GDP-mannose-linker-ApoE

a-i = 0; q (independently selected) = 0 or 1; z = 1;  
r-u (independently selected) = 0 or 1;  
j-m (independently selected) = 0-100;  
Sia = mannose or mannose with mannose-6-phosphate;  
v-y (independently selected) = 0 or 1;  
R = mannose-linker-ApoE.

FIG. 56F

CHO, BHK, 293 cells, Insect cells, Vero, yeast,  
fungi expressed alpha-galactosidase.  
a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;  
r-u (independently selected) = 0 or 1;  
j-m (independently selected) = 0-100;  
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. endo-H  
2. galactosyltransferase,  
UDP-Gal-linker-alpha2-macroglobulin

a-m, r-z = 0; n, q (independently selected) = 0 or 1;  
R' = galactose-linker-alpha2-macroglobulin.

FIG. 56G



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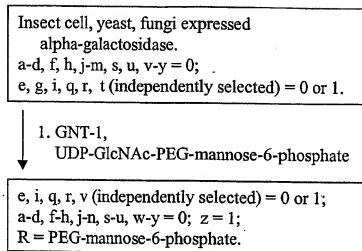


FIG. 56H

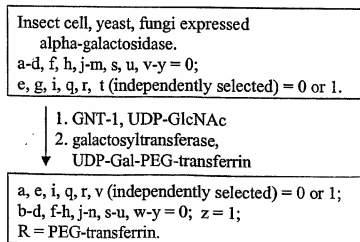


FIG. 56I

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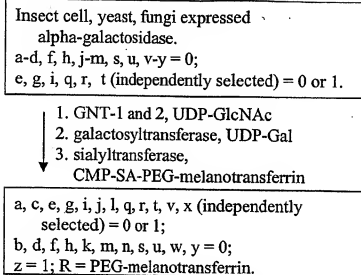
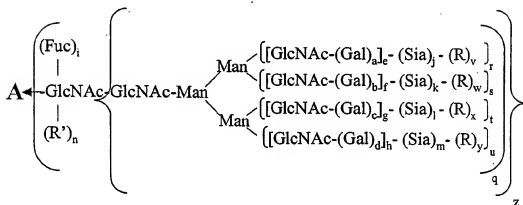
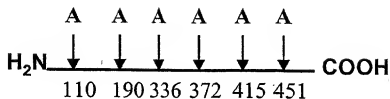


FIG. 56J

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a-d, i, n, q-u, z (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0 to 100;

R = mannose, mannose-6-phosphate and mannose, polymer.

FIG. 57A

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CHO, BHK, 293 cells, Insect cells, Vero expressed  
and secreted alpha-iduronidase  
a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;  
n, v-y = 0; and when a-n = 0, then r-u (independently  
selected) = 0 or 1; v-y (independently selected) = 0-100;  
R = mannose or mannose with mannose-6-phosphate.

- ↓  
1. Endo-H  
↓  
2. Galactosyltransferase, UDP-Gal-PEG-transferrin

a-h, i-m, q-u (independently selected) = 0 or 1;  
n, v-y = 0; z = 1; and when z = 0 and q = 1, then n  
(independently selected) = 0 or 1; R' = Gal-PEG-transferrin.

FIG. 57B

CHO, BHK, 293 cells, Insect cells, Vero expressed  
and secreted alpha-iduronidase  
a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;  
n, v-y = 0; and when a-n = 0, then r-u (independently  
selected) = 0 or 1; v-y (independently selected) = 0-100;  
R = mannose or mannose with mannose-6-phosphate.

- ↓  
1. Sialidase  
↓  
2. CMP-SA-linker-Mannose-6-phosphate ST3Gal3

a-h, i-m, q-u, v-y (independently selected) = 0 or 1; n = 0;  
z = 1; R = mannose-6-phosphate; and when a-n = 0,  
then r-u (independently selected) = 0 or 1;  
v-y (independently selected) = 0-100;  
R = mannose or mannose with mannose-6-phosphate.

FIG. 57C

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NSO expressed alpha-iduronidase.

a-d, i-m, q-u (independently selected) = 0 or 1; e-h = 1;

v-y = 0; Sia (independently selected) = Sia or Gal.

↓ 1. Sialidase and  $\alpha$ -galactosidase

2. Galactosyltransferase, UDP-Gal

↓ 3. CMP-SA-linker-mannose-6-phosphate sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = mannose-6 phosphate

FIG. 57D

CHO, BHK, 293 cells, Insect cells, Vero expressed  
and secreted alpha-iduronidase

a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;

n, v-y = 0; and when a-n = 0, then r-u (independently

selected) = 0 or 1; v-y (independently selected) = 0-100;

R = mannose or mannose with mannose-6-phosphate.

↓ 1. Sialidase

2. CMP-SA-PEG, sialyltransferase

a-h, i-m, q-u, v-y (independently selected) = 0 or 1; n = 0;

z = 1; R = PEG; and when a-n = 0, then r-u

(independently selected) = 0 or 1; v-y = 0-100;

R = mannose or mannose with mannose-6-phosphate.

FIG. 57E

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CHO, BHK, 293 cells, Insect cells, Vero, yeast, fungi  
expressed alpha-iduronidase.  
a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;  
r-u (independently selected) = 0 or 1;  
j-m (independently selected) = 0-100;  
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. mannosyltransferase,  
GDP-mannose-linker-ApoE

a-i = 0; q (independently selected) = 0 or 1; z = 1;  
r-u (independently selected) = 0 or 1; j-m (independently  
selected) = 0-100;  
Sia = mannose or mannose with mannose-6-phosphate;  
v-y (independently selected) = 0 or 1;  
R = mannose-linker-ApoE.

FIG. 57F

CHO, BHK, 293 cells, Insect cells, Vero, yeast, fungi  
expressed alpha-iduronidase.  
a-i, v-y = 0; q (independently selected) = 0 or 1;  
z = 1; r-u (independently selected) = 0 or 1;  
j-m (independently selected) = 0-100;  
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. endo-H  
2. galactosyltransferase,  
UDP-Gal-linker-alpha2-macroglobulin

a-m, r-z = 0; n, q (independently selected) = 0 or 1;  
R' = galactose-linker-alpha2-macroglobulin.

FIG. 57G

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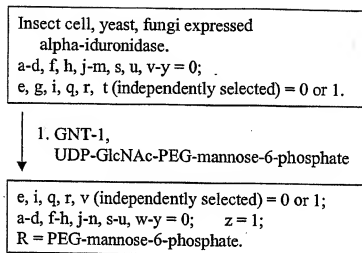


FIG. 57H

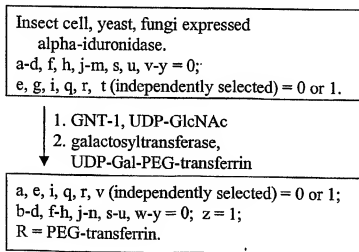


FIG. 57I

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Insect cell, yeast, fungi expressed  
alpha-iduronidase.

a-d, f, h, j-m, s, u, v-y = 0;

c, g, i, q, r, t (independently selected) = 0 or 1.

- ↓  
1. GNT-1 and 2, UDP-GlcNAc  
2. galactosyltransferase, UDP-Gal  
3. sialyltransferase,  
CMP-SA-PEG-melanotransferrin

a, c, e, g, i, j, l, q, r, t, v, x

(independently selected) = 0 or 1;

b, d, f, h, k, m, n, s, u, w, y = 0; z = 1;

R = PEG-melanotransferrin.

FIG. 57J



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FIG. 58A

ACCCCCCTGGGCCCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAT  
GCTTAGAGCAAGTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAG  
GAGAAGCTGTGTGCCACCTACAAGCTGTGCCACCCCGAGGAGCTGGT  
GCTGCTCGGACACTCTCTGGGCATCCCTGGGCTCCCTTGAGCAGCTG  
CCCCAGCCAGGCCCTGCAGCTGGCAGGCTGCTTGAGCCAACTCCATA  
GCGGCCTTTTCCTCTACCAGGGGCTCCTGCAGGCCCTGGAAGGGATCT  
CCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTGGACGTCGCCG  
ACTTTGCCACCACCATCTGGCAGCAGATGGAAGAACTGGGAATGGCC  
CCTGCCCTGCAGCCCACCCAGGGTGCCATGCCGGCCTTCGCCTCTGCT  
TTCCAGCGCCGGGCAGGAGGGGTCCTGGTTGCCTCCCATCTGCAGAG  
CTTCTGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCCAGCCCTG  
A

FIG. 58B

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu  
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr  
Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro  
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser  
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile  
Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe  
Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro  
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val  
Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His  
Leu Ala Gln Pro

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FIG. 59A

GCGCCTCTTATGTACCCACAAAAATCTATTTTCAAAAAAGTTGCTCTA  
AGAAATATAGTTATCAAGTTAAGTAAAATGTCAATAGCCTTTTAATTTA  
ATTTTAAATTGTTTTATCATTCTTTGCAATAATAAACATTAACTTTAT  
ACTTTTAAATTATATAGAAATAGAGATATACATAGGATATGTAAA  
TAGATACACAGTGTATATGTGATTAAAAATATAATGGGAGATTCAATC  
AGAAAAAAGTTTCTAAAAAGGCTCTGGGGTAAAAGAGGAAGGAAAC  
AATAATGAAAAAATGTGGTGAGAAAAACAGCTGAAAACCCATGTA  
AAGAGTGATAAAGAAAGCAAAAAGAGAAGTAGAAAAGTAACACAGG  
GGCATTGTGGAAATGTAAACGAGTATGTTCCCTATTTAAGGCTAGGC  
ACAAAGCAAGGTCTTCAGAGAACCTGGAGCCTAAGGTTTAGGCTCAC  
CCATTTCAACCAGTCTAGCAGCATCTGCAACATCTACAATGGCCTTGA  
CCTTTGCTTTACTGGTGGCCCTCCTGGTGCTCAGCTGCAAGTCAAGCT  
GCTCTGTGGGCTGTGATCTGCCTCAAACCCACAGCTGGGTAGCAGG  
AGGACCTTGATGCTCCTGGCACAGATGAGGAGAATCTCTTTTCTCC  
TGCTTGAAGGACAGACATGACTTTGGATTTCCTCAGGAGGAGTTTGG  
CAACCAGTTCAAAAGGCTGAAACCATCCCTGTCTCCATGAGATGA  
TCCAGCAGATCTTCAATCTCTTCAGCACAAAGGACTCATCTGCTGCTT  
GGGATGAGACCTCCTAGACAAAATTCTACACTGAACTCTACCAGCAG  
CTGAATGACCTGGAAGCCTGTGTGATACAGGGGGTGGGGGTGACAGA  
GACTCCCCTGATGAAGGAGGACTCCATTCTGGCTGTGAGGAAATACT  
TCCAAAGAATCACTCTCTATCTGAAAGAGAAGAAATACAGCCCTTGT  
GCCTGGGAGGTTGTGAGAGCAGAAATCATGAGATCTTTTTCTTTGTCA  
ACAAACTGTGAAGAAAGTTTAAGAAGTAAGGAATGAAAACCTGGTTCA  
ACATGGAAATGATTTTCATTGATTCGTATGCCAGCTACCTTTTTATG  
ATCTGCCATTTCAAAGACTCATGTTTCTGCTATGACCATGACACGATT  
TAAATCTTTTCAAATGTTTTTAGGAGTATTAATCAACTATTGTATTCAG  
CTCTTAAGGCACTAGTCCCTTACAGAGGACCATGCTGACTGATCCATT  
ATCTATTTAAATATTTTTAAAAATATTATTTATTTAACTATTTATAAAAC  
AACTTATTTTGTTCATATTATGTCATGTGCACCTTTGCACAGTGGTTA  
ATGTAATAAAATGTGTTCTTTGTATTTGGTAAATTTATTTTGTGTTGTT  
CATTGAACCTTTTGTATGGAACCTTTGTACTTGTTTATCTTTTAAATG  
AAATCCAAGCCTAATTGTGCAACCTGATTACAGAATAACTGGTACA  
CTTCACTTTGTCCATCAATATTATATTCAAGATATAAGTAAAAATAAAC  
TTTCTGTAAACCAAGTTGTATGTTGTACTCAAGATAACAGGGTGAACC  
TAACAAATACAATTCTGCTCTCTCTGTGTATTTGATTTTGTATGAAAA  
AAACTAAAAATGGTAATCATACTTAATTATCAGTTATGGTAAATGGT  
ATGAAGAGAAGAAGGAACG

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## FIG. 59B

Met Ala Leu Thr Phe Ala Leu Leu Val Ala Leu Leu Val Leu Ser Cys Lys Ser  
 Ser Cys Ser Val Gly Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr  
 Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp  
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln Lys Ala  
 Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr  
 Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu  
 Leu Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val  
 Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe  
 Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val  
 Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser Leu  
 Arg Ser Lys Glu

## FIG. 59C

ATGGCCCTCCTGTTCCCTCTACTGGCAGCCCTAGTGATGACCAGCTAT  
 AGCCCTGTTGGATCTCTGGGCTGTGATCTGCCTCAGAACCATGGCCTA  
 CTTAGCAGGAACACCTTGTTGCTTCTGCACCAAATGAGGAGAATCTCC  
 CCTTTCTGTGTCTCAAGGACAGAAGAGACTTCAGGTTCCCCAGGAG  
 ATGGTAAAAGGGAGCCAGTTGCAGAAGGCCCATGTTCATGTCTGTCT  
 CCATGAGATGCTGCAGCAGATCTTCAGCCTCTTCCACACAGAGCGCTC  
 CTCTGCTGCCTGGAACATGACCCTCTAGACCAACTCCACACTGGACT  
 TCATCAGCAACTGCAACACCTGGAGACCTGCTTGCTGCAGGTAGTGG  
 GAGAAGGAGAAATCTGCTGGGGCAATTAGCAGCCCTGCACCTGACCTTG  
 AGGAGGTACTTCCAGGGAATCCGTGTCTACCTGAAAGAGAAGAAATA  
 CAGCGACTGTGCCTGGGAAGTTGTGAGAATGGAAATCATGAAATCCT  
 TGTTCCTTATCAACAAACATGCAAGAAAGACTGAGAAGTAAAGATAGA  
 GACCTGGGCTCATCTTGA

## FIG. 59D

Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr Ser Pro Val  
 Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu Leu Ser Arg Asn Thr  
 Leu Val Leu Leu His Gln Met Arg Arg Ile Ser Pro Phe Leu Cys Leu Lys Asp  
 Arg Arg Asp Phe Arg Phe Pro Gln Glu Met Val Lys Gly Ser Gln Leu Gln Lys  
 Ala His Val Met Ser Val Leu His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His  
 Thr Glu Arg Ser Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr  
 Gly Leu His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly  
 Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg Arg Tyr Phe  
 Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser Asp Cys Ala Trp Glu Val  
 Val Arg Met Glu Ile Met Lys Ser Leu Phe Leu Ser Thr Asn Met Gln Glu Arg  
 Leu Arg Ser Lys Asp Arg Asp Leu Gly Ser Ser

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FIG. 60A

ATGACCAACAAGTGTCTCTCTCCAAATTGCTCTCCTGTTGTGCTTCTCC  
 ACTACAGCTCTTTCCATGAGCTACAACCTTGCTTGGATTCTACAAAGA  
 AGCAGCAATTTTCAGTGTGAGAAGCTCCTGTGGCAATTGAATGGGAG  
 GCTTGAATATTGCCTCAAGGACAGGATGAACCTTGACATCCCTGAGG  
 AGATTAAGCAGCTGCAGCAGTTCCAGAAGGAGGACGCCGATTGACC  
 ATCTATGAGATGCTCCAGAACATCTTTGCTATTTTCAGACAAGATTCA  
 TCTAGCACTGGCTGGAATGAGACTATTGTTGAGAACCTCCTGGCTAA  
 TGTCTATCATCAGATAAACCATCTGAAGACAGTCTTGAAGAAAAAC  
 TGGAGAAAGAAGATTTTACCAGGGGAAAACATGAGCAGTCTGCAC  
 CTGAAAAGATATTATGGGAGGATTCTGCATTACCTGAAGGCCAAGGA  
 GTACAGTCACTGTGCCTGGACCATAGTCAGAGTGGAAATCCTAAGGA  
 ACTTTTACTTCATTAACAGACTTACAGGTTACCTCCGAAACTGAAGAT  
 CTCCTAGCCTGTCCCTCTGGGACTGGACAATTGCTCAAGCATTCTTC  
 AACCAGCAGATGCTGTTTAAGTGACTGATGGCTAATGTACTGCAAAAT  
 GAAAGGACACTAGAAGATTTTGAAATTTTATTAAATTATGAGTTATT  
 TTTATTTAT TTAATTTTATTTTGGAAAAATAAATTATTTTGGTGC

FIG. 60B

Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser Thr Thr Ala  
 Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln  
 Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp  
 Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu  
 Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln  
 Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val  
 Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp  
 Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile  
 Leu His Tyr Leu Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val  
 Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn

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FIG. 61A

ATGGTCTCCCAGGCCCTCAGGCTCCTCTGCCTTCTGCTTGGGCTTCAG  
GGCTGCCTGGCTGCAGTCTTCGTAACCCAGGAGGAAGCCCACGGCGT  
CCTGCACCGGCGCCGGCGCGCCAACGCGTTCTTGAGGAGCTGCGGG  
CGGGCTCCCTGGAGAGGGAGTGCAAGGAGGAGCAGTGCTCCTTCGA  
GGAGGCCCGGGAGATCTTCAAGGACGCGGAGAGGACGAAGCTGTTC  
TGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCA  
GAATGGGGGCTCCTGCAAGGACCAGTCCAGTCCATATATCTGCTTCT  
GCCTCCCTGCCTTCGAGGGCCGGAACCTGTGAGACGCACAAGGATGAC  
CAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAGCAGTACTGCAG  
TGACCACACGGGCACCAAGCGCTCCTGTGCGGTGCCACGAGGGGTACT  
CTCTGCTGGCAGACGGGGTGTCTGCACACCCACAGTTGAATATCCA  
TGTGGAATAATACCTATTCTAGAAAAAAGAAATGCCAGCAAAACCCCA  
AGGCCGAATTGTGGGGGGCAAGGTGTGCCCAAAGGGGAGTGTCCA  
TGGCAGGTCTCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGGGGGGAC  
CCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAA  
AATCAAGAACTGGAGGAACCTGATCGCGGTGTCTGGGCGAGCACGAC  
CTCAGCGAGCACGACGGGGATGAGCAGAGCCGGCGGGTGGCGCAGG  
TCATCATCCCCAGCACGTACGTCCCGGGCACCAACCAACACGACATC  
GCGCTGCTCCGCCTGCACCAGCCCGTGGTCCTCACTGACCATGTGGTG  
CCCCTCTGCCTGCCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTC  
GTGCTCTTCTCATTTGGTCAGCGGCTGGGGCCAGCTGCTGGACCGTGG  
CGCCACGGCCCTGGAGCTCATGGTGTCTCAACGTGCCCGGCTGATGA  
CCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGGAGACTCCCCAAAT  
ATCAGGAGTACATGTTCTGTGCCGCTACTCGGATGGCAGCAAGGA  
CTCCTGCAAGGGGGACAGTGGAGGCCACATGCCACCCACTACCGGG  
GCACGTGGTACCTGACGGGCATCGTACGTGGGGCCAGGGCTGCGCA  
ACCGTGGGGCACTTTGGGGTGTACACCAGGGTCTCCAGTACATCGA  
GTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCCAGGAGTCTCTC  
TGCGAGCCCCATTCCC

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FIG. 61B

Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln Gly Cys  
Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val Leu His Arg Arg Arg  
Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys  
Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg  
Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys  
Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro  
Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val  
Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg  
Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro  
Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys  
Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln  
Val Leu Leu Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile  
Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile  
Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg  
Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His Asp  
Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His Val Val Pro Leu  
Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser  
Leu Val Ser Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu  
Met Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg  
Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp  
Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg  
Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala Thr Val Gly  
His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met  
Arg Ser Glu Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro

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FIG. 62A

ATGCAGCGCGTGAACATGATCATGTCGAGAAATCACCAAGCCTCATCAC  
CATCTGCCTTTTAGGATATCTACTCAGTGCTGAAATGTACAGTTTTTCTT  
GATCATGAAAAACGCCAACAAAAATCTGAATCGGCCAAAAGAGGTATAA  
TTCAGGTAAATTTGGAAGAGTTTGTTCAGGGAACCTTGAGAGAGAAT  
GTATGGAAGAAAAGTGTAGTTTTGAAGAACCACGAGAAGTTTTTGAA  
AACACTGAAAAGACAACCTGAATTTTGGAAGCAGTATGTTGATGGAGA  
TCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATG  
ACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTGGAAGGAAAGA  
ACTGTGAATTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAG  
CAGTTTTGTAAAAATAGTGCTGATAACAAGGTGGTTTGCTCCTGTACT  
GAGGGATATCGACTTGCAGAAAACCAGAAATCCTGTGAACCAGCAGT  
GCCATTTCCATGTGGAAGAGTTTCTGTTTCAAAACTTCTAAGCTCAC  
CCGTGCTGAGGCTGTTTTTCTGTATGTGGACTATGTAATCCTACTGA  
AGCTGAAACCATTTTGGATAACATCACTCAAGGCACCCAATCATTTA  
ATGACTTCACTCGGGTGTGTGGTGGAGAAGATGCCAAACCAGGTCAA  
TTCCCTTGGCAGGTGTTTTGAATGGTAAAGTTGATGCATTCTGTGGA  
GGCTCTATCGTTAATGAAAAATGGATTGTAACCTGCTGCCACTGTGTT  
GAAACTGGTGTAAAAATTACAGTTGTCGCAGGTGAACATAATATTGA  
GGAGACAGAAACATACAGAGCAAAAGCGAAATGTGATTCGAGCAATT  
ATTCTCACCACACTACAATGCAGCTATTAATAAGTACAACCATGA  
CATTGCCCTTCTGGAACCTGGACGAACCCCTAGTGTCAAAACAGCTACG  
TTACACCTATTTCGATTGCTGACAAGGAATACACGAACATCTTCTCA  
AATTGGATCTGGCTATGTAAGTGGCTGGGCAAGAGTCTTCCACAAA  
GGGAGATCAGCTTTAGTTCTTCAGTACCTTAGAGTTCCACTTGTGAC  
CGAGCCACATGCTTCGATCTACAAAGTTACCATCTATAACAACAT  
GTTCTGTGCTGGCTTCCATGAAGGAGGTAGAGATTCATGTCAAGGAG  
ATAGTGGGGGACCCCATGTTACTGAAGTGGAAGGGACCAGTTTCTTA  
ACTGGAATTATTAGCTGGGGTGAAGAGTGTGCAATGAAAGGCAAAATA  
TGGAATATATACCAAGGTATCCCGGTATGTCAACTGGATTAAAGGAAA  
AAACAAAGCTCACITTAATGAAAGATGGATTTCGAAGGTTAATTCATT  
GGAATTGAAAATTAACAG

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FIG. 62B

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Ser Leu Ile Thr Ile Cys Leu  
Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu Asp His Glu Asn Ala  
Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn Ser Gly Lys Leu Glu Glu Phe  
Val Gln Gly Asn Leu Glu Arg Glu Cys Met Glu Glu Lys Cys Ser Phe Glu Glu  
Pro Arg Glu Val Phe Glu Asn Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr  
Val Asp Gly Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys  
Asp Asp Ile Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn  
Cys Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe Cys  
Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly Tyr Arg Leu  
Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe Pro Cys Gly Arg Val Ser  
Val Ser Gln Thr Ser Lys Leu Thr Arg Ala Glu Ala Val Phe Pro Asp Val Asp Tyr  
Val Asn Pro Thr Glu Ala Glu Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser  
Phe Asn Asp Phe Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe  
Pro Trp Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile Val  
Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly Val Lys Ile Thr  
Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu His Thr Glu Gln Lys Arg Asn  
Val Ile Arg Ala Ile Ile Pro His His Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn  
His Asp Ile Ala Leu Leu Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr  
Pro Ile Cys Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly  
Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu Val Leu Gln  
Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Arg Ser Thr Lys Phe  
Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His Glu Gly Gly Arg Asp Ser  
Cys Gln Gly Asp Ser Gly Gly Pro His Val Thr Glu Val Glu Gly Thr Ser Phe Leu  
Thr Gly Ile Ile Ser Trp Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr  
Thr Lys Val Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr



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FIG. 63A

ATGGATTACTACAGAAAATATGCAGCTATCTTTCTGGTCACATTGTCTG  
GTGTTTCTGCATGTTCTCCATTCCGCTCCTGATGTGCAGGATTGCCCA  
GAATGCACGCTACAGGAAAACCCATTCTTCTCCAGCCGGGTGCCCC  
AATACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCC  
ACTAAGGTCCAAGAAGACGATGTTGGTCCAAAAGAACGTACCTCAG  
AGTCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCACAGTAATG  
GGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTG  
TTATTATCACAAATCTTAAATGTTTTACCAAGTGCTGTCTTGATGACT  
GCTGATTTTCTGGAATGGAAAATTAAGTTGTTTAGTGTTTATGGCTTT  
GTGAGATAAACTCTCCTTTTCCTTACCATACCACTTTGACACGCTTC  
AAGGATATACTGCAGCTTTACTGCCTTCCCTCCTTATCCTACAGTACAA  
TCAGCAGTCTAGTTCTTTTCATTTGGAATGAATACAGCATTAAGCTTG  
TTCCACTGCAAATAAAGCCTTTTAAATCATC

FIG. 63B

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser Val Phe Leu  
His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu  
Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe  
Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn  
Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met  
Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His  
Lys Ser

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FIG. 63C

ATGAAGACACTCCAGTTTTTCTTCCTTTTCTGTTGCTGGAAAGCAATC  
TGCTGCAATAGCTGTGAGCTGACCAACATCACCATTGCAATAGAGAA  
AGAAGAATGTCGTTTCTGCATAAGCATCAACACCACTTGGTGTGCTG  
GCTACTGCTACACCAGGGATCTGGTGTATAAGGACCCAGCCAGGCCC  
AAAATCCAGAAAACATGTACCTTCAAGGAACTGGTATATGAAACAGT  
GAGAGTGCCCGGCTGTGCTCACCATGCAGATTCCTTGTATACATACCC  
AGTGGCCACCCAGTGTCACTGTGGCAAGTGTGACAGCGACAGCACTG  
ATTGTA CTGTGCGAGGCCTGGGGCCAGCTACTGCTCCTTTGGTGAAA  
TGAAAGAATAA

FIG. 63D

Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile Cys Cys  
Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys Glu Glu Cys Arg Phe  
Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly Tyr Cys Tyr Thr Arg Asp Leu Val  
Tyr Lys Asp Pro Ala Arg Pro Lys Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val  
Tyr Glu Thr Val Arg Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr  
Pro Val Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys  
Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys Glu

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FIG. 64A

CCCGGAGCCGGACCGGGGCCACCGCGCCCGCTCTGCTCCGACACCGC  
GCCCCCTGGACAGCCGCCCTCTCCTCCAGGCCCGTGGGGCTGGCCCT  
GCACCGCCGAGCTTCCCCGGATGAGGGCCCCCGGTGTGGTCACCCGG  
CGCGCCCCAGGTGCTGCTGAGGGACCCCGGCCAGGCGCGGAGATGGGG  
GTGCACGAATGTCCTGCTGGCTGTGGCTTCTCCTGTCCCTGCTGTGCTG  
CTCCTCTGGGCCCTCCAGTCTCTGGGCGCCCCACCACGCCTCATCTGT  
GACAGCCGAGTCTCTGGAGAGGTACCTCTTGGAGGCCAAGGAGGCCG  
AGAATATCACGACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAAT  
ATCACTGTCCCAGACACCAAAGTTAATTTCTATGCCTGGAAAGGAT  
GGAGGTCGGGCAGCAGGCCGTAGAAGTCTGGCAGGGCCTGGCCCTG  
CTGTCGGAAGCTGTCCTGCGGGGCCAGGCCCTGTTGGTCAACTCTTCC  
CAGCCGTGGGAGCCCCCTGCAGCTGCATGTGGATAAAGCCGTCAGTGG  
CCTTCGCAGCCTCACCACTCTGCTTCGGGCTCTGCGAGCCAGAAGG  
AAGCCATCTCCCCCTCCAGATGCGGCCTCAGCTGCTCCACTCCGAACA  
ATCACTGCTGACACTTTCGCAAACTCTTCCGAGTCTACTCCAATTTCT  
CTCCGGGAAAGCTGAAGCTGTACACAGGGGAGGCCTGCAGGACAG  
GGGACAGATGACCAGGTGTGTCCACCTGGGCATATCCACCACCTCCC  
TCACCAACATTGCTGTGTGCCACACCCCTCCCCCGCCACTCCTGAACCCC  
GTGAGGGGCTCTCAGCTCAGCGCCAGCCTGTCCCATGGACACTCCA  
GTGCCAGCAATGACATCTCAGGGGCCAGAGGAACTGTCCAGAGAGC  
AACTCTGAGATCTAAGGATGTACAGGGCCAACTTGAGGGCCAGAG  
CAGGAAGCATTAGAGAGCAGCTTTAAACTCAGGGACAGGCCATG  
CTGGGAAGACGCCTGAGCTCACTCGGCACCCTGCAAAATTTGATGCC  
AGGACACGCTTTGGAGGCGATTTACCTGTTTTCGCACCTACCATCAGG  
GACAGGATGACCTGGGAACTTAGGTGGCAAGCTGTGACTTCTCCAG  
GTCTCACGGGCATGGGCACTCCCTTGGTGGCAAGAGCCCCCTTGACA  
CCGGGGTGGTGGGAACCATGAAGACAGGATGGGGGCTGGCCCTCTGG  
CTCTCATGGGGTCCAAGTTTGTGTATTCTTCAACCTCATTGACAAGA  
ACTGAAACCACCAAAAAAAAAAAAAA

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FIG. 64B

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Ser Leu Leu Ser  
Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu Ile Cys Asp Ser  
Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr  
Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys  
Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val  
Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu  
Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser  
Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu Ala Ile  
Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe  
Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr  
Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg

FIG. 65

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala  
Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn  
Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly  
Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg  
Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val  
Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly  
Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr  
Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly  
Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp

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FIG. 66A

ATGTGGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCAT  
CTCTGCACCCGCCCCGCTCGCCAGCCCCAGCACGCAGCCCTGGGAGC  
ATGTGAATGCCATCCAGGAGGCCGCGTCTCCTGAACCTGAGTAGA  
GACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAGAAAAT  
GTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGT  
ACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTG  
ACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGA  
AACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGA  
ACCTGAAGGACTTTCTGCTTGTATCCCCTTTGACTGCTGGGAGCCAG  
TCCAGGAGTGA

FIG. 66B

Met Trp Leu Gln Ser Leu Leu Leu Gly Thr Val Ala Cys Ser Ile Ser Ala Pro  
Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His Val Asn Ala Ile Gln Glu  
Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp Thr Ala Ala Glu Met Asn Glu Thr  
Val Glu Val Ile Ser Glu Met Phe Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg  
Leu Glu Leu Tyr Lys Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro  
Leu Thr Met Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser  
Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys Asp Phe Leu  
Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu

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FIG. 67A

ATGAAATATACAAGTTATATCTTGCTTTTCAGCTCTGCATCGTTTGG  
 GGTTCCTCTTGCTGTTACTGCCAGGACCCATATGTAAAAAGAAGCAGA  
 AAACCTTAAGAAATATTTTAATGCAGGTCATTTCAGATGTAGCGGATA  
 ATGGAACCTCTTTTCTTAGGCATTTTGAAGAATTGGAAAGAGGAGAGT  
 GACAGAAAAATAATGCAGAGCCAAATTGTCTCCTTTTACTTCAAACT  
 TTTTAAAAACTTTAAAGATGACCAGAGCATCCAAAAGAGTGTGGAGA  
 CCATCAAGGAAGACATGAATGTCAAGTTTTTCAATAGCAACAAAAAG  
 AAACGAGATGACTTCGAAAAGCTGACTAATTATTCGGTAACTGACTT  
 GAATGTCCAACGCAAAGCAATACATGAACTCATCCAAGTGATGGCTG  
 AACTGTGCGCCAGCAGCTAAAAACAGGGAAGCGAAAAAGGAGTCAGAT  
 GCTGTTTCGAGGTGCAAGAGCATCCCAAGTAA

FIG. 67B

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu Gly Ser Leu  
 Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr  
 Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile  
 Leu Lys Asn Trp Lys Glu Ser Asp Arg Lys Ile Met Gln Ser Gln Ile Val Ser  
 Phe Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val  
 Gly Thr Ile Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys  
 Arg Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val Gln  
 Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser Pro Ala Ala Lys  
 Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg Gly Arg Arg Ala Ser Gln

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FIG. 68A

CTGGGACAGTGAATCGACAATGCCGTCTTCTGTCTCGTGGGGCATCCT  
CCTGCTGGCAGGCCTGTGCTGCCTGGTCCCTGTCTCCCTGGCTGAGGA  
TCCCCAGGGAGATGCTGCCCAGAAGACAGATACATCCCACCATGATC  
AGGATCACCCAACCTTCAACAAGATCACCCCCAACCTGGCTGAGTTC  
GCCTTCAGCCTATACCGCCAGCTGGCACACCAGTCCAACAGCACCAA  
TATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTC  
CCTGGGGACCAAGGCTGACACTCACGATGAAATCCTGGAGGGCCTGA  
ATTTCAACCTCACGGAGATTCCGGAGGCTCAGATCCATGAAGGCTTC  
CAGGAACTCCTCCGTACCCTCAACCAGCCAGACAGCCAGCTCCAGCT  
GACCACCGGAATGGCCTGTTCTCAGCGAGGGCCTGAAGCTAGTGG  
ATAAGTTTTTGGAGGATGTTAAAAAGTTGTACCACTCAGAAAGCCTTC  
ACTGTCAACTTCGGGGACACCGAAGAGGCCAAGAAACAGATCAACG  
ATTACGTGGAGAAGGGTACTCAAGGGAATTTGTGGATTTGGTCAAG  
GAGCTTGACAGAGACACAGTTTTTGTCTCTGGTGAATTACATCTTCTTT  
AAAGGCAAAATGGGAGAGACCCCTTTGAAGTCAAGGACACCGAGGAAG  
AGGACTTCCACGTGGACCAGGTGACCACCGTGAAGGTGCCTATGATG  
AAGCGTTTAGGCATGTTTAACATCCAGCACTGTAAGAAGCTGTCCAG  
CTGGGTGCTGCTGATGAAATACCTGGGCAATGCCACCGCCATCTTCT  
TCCTGCCTGATGAGGGGAAACTACAGCACCTGGAAAATGAACTCACC  
CACGATATCATCACCAAGTTTCTGGAAAATGAAGACAGAAGGTCTGC  
CAGCTTACATTACCCAACTGTCCATTACTGGAACCTATGATCTGAA  
GAGCGTCTGGGTCAACTGGGCATCACTAAGGTCTTCAGCAATGGGG  
CTGACCTCTCCGGGGTACAGAGGAGGCACCCCTGAAGCTCTCCAAG  
GCCGTGCATAAGGCTGTGCTGACCATCGACGAGAAAAGGACTGAAGC  
TGCTGGGGCCATGTTTTAGAGGCCATACCCATGTCTATCCCCCGGA  
GGTCAAGTTCAACAAACCCTTTGTCTTCTTAATGATTGAACAAAAATAC  
CAAGTCTCCCCTCTTCATGGGAAAAGTGGTGAATCCCACCCAAAAAT  
AACTGCCTCTCGTCTCTCAACCCCTCCCCTCCATCCCTGGCCCCCTCC  
CTGGATGACATTAAAGAAGGGTTGAGCTGG

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FIG. 68B

Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val  
Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr Asp Thr Ser  
His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr Pro Asn Leu Ala Glu Phe  
Ala Phe Ser Leu Tyr Arg Gln Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe  
Ser Pro Val Ser Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp  
Thr His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala  
Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln  
Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu Val  
Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala Phe Thr Val  
Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys  
Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val  
Phe Ala LeuVal Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val  
Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val  
Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser  
Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu Pro  
Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp Ile Ile Thr Lys  
Phe Leu Glu Asn Glu AspArg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile  
Thr Gly Thr Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe  
Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys  
Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala  
Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu Val Lys Phe Asn Lys Pro  
Phe Val Phe Leu Met Ile Glu Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val  
Val Asn Pro Thr Gln Lys



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FIG. 69A-1

GCTAACCTAGTGCCTATAGCTAAGGCAGGTACCTGCATCCTTGTTTT  
GTTTAGTGGATCCTCTATCCTTCAGAGACTCTGGAACCCCTGTGGTCT  
TCTCTTCATCTAATGACCCTGAGGGGATGGAGTTTTC AAGTCCTTCCA  
GAGAGGAATGTCCCAAGCCTTTGAGTAGGGTAAGCATCATGGCTGGC  
AGCCTCACAGGTTTGCTTCTACTTCAGGCAGTGTCTGTGGCATCAGGT  
GCCCCCCCCTGCATCCCTAAAAGCTTCGGCTACAGCTCGGTGGTGTGT  
GTCTGCAATGCCACATACTGTGACTCCTTTGACCCCCGACCTTTCCT  
GCCCTTGGTACCTTCAGCCGCTATGAGAGTACACGCAGTGGGCGACG  
GATGGAGCTGAGTATGGGGCCCATCCAGGCTAATCACACGGGCACAG  
GCCTGCTACTGACCCTGCAGCCAGAACAGAAGTCCAGAAAAGTGAAG  
GGATTGGAGGGGCCATGACAGATGCTGCTGCTCTCAACATCCTTGCC  
CTGTACACCCCTGCCCAAAATTTGCTACTTAAATCGTACTTCTCTGAA  
GAAGGAATCGGATATAACATCATCCGGGTACCCATGGCCAGCTGTGA  
CTTCTCCATCCGCACCTACACCTATGCAGACACCCCTGATGATTTCCA  
GTTGCACAACCTCAGCCTCCCAGAGGAAGATACCAAGCTCAAGATAC  
CCCTGATTACCCGAGCCCTGCAGTTGGCCAGCGTCCGTTTCACTCC  
TTGCCAGCCCCCTGGACATCACCCACTTGGCTCAAGACCAATGGAGCG  
GTGAATGGGAAGGGGTCACTCAAGGACAGCCCGGAGACATCTACC  
ACCAGACCTGGGCCAGATACTTTGTGAAGTTCCTGGATGCCTATGCTG  
AGCACAAGTATACAGTTCTGGGCAGTGACAGCTGAAAATGAGCCTTCT  
GCTGGGCTGTTGAGTGGATACCCCTTCCAGTGCCTGGGCTTACCCCT  
GAACATCAGCGAGACTTCATTGCCCGTGACCTAGGTCTTACCCTCGCC  
AACAGTACTCACCACAATGTCCGCCTACTCATGCTGGATGACCAACCG  
TTGCTGCTGCCCCACTGGGCAAAGGTGGTACTGACAGACCCAGAAGC  
AGCTAAATATGTTTCATGGCATTGCTGTACATTGGTACTGGACTTTCT  
GGCTCCAGCCAAAGCCACCCTAGGGGAGACACACCGCCTGTTCCCCA  
ACACCATGCTCTTTGCCTCAGAGGCCCTGTGTGGGCTCCAAGTTCTGGG  
AGCAGAGTGTGCGGCTAGGCTCCTGGGATCGAGGGATGCAGTACAGC  
CACAGCATCATCAGAACCTCCTGTACCATGTGTGCGGTGGACCGAG  
TGGAACCTTGCCCTGAACCCCGAAGGAGGACCCAATTGGGTGCGTAA  
CTTGTGCGACAGTCCCATCATTGTAGACATCACC AAGGACAGGTTTAA  
CAAACAGCCCATGTTCTACCACCTTGGCCACTTCAGCAAGTTCATTCC  
TGAGGGCTCCCAAGAGAGTGGGGCTGGTTGCCAGTCAGAAGAACGACC  
TGGACGCAGTGGCAGTGTGATGCATCCCGATGGCTGTCTGTTGTGGTCTG  
TGCTAAACCGCTCCTCTAAGGATGTGCCTCTTACCATCAAGGATCCTG  
CTGTGGGCTTCTCGAGACAATCTCACCTGGCTACTCCATTCAACCT  
ACCTGTGGCATCGCCAGTGATGGAGCAGATACTCAAGGAGGCACTGG  
GCTCAGCCTGGGCATTAAAGGGACAGAGTCAGCTCACACGCTGTCTG  
TGACTAAAGAGGGCACAGCAGGGCCAGTGTGAGCTTACAGCGACGT

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FIG. 69A-2

AAGCCCAGGGGCAATGGTTTGGGTGACTCACTTTCCTCTAGGTGGT  
 GCCCAGGGCTGGAGGCCCTAGAAAAAGATCAGTAAGCCCCAGTGTG  
 CCCCCAGCCCCCATGCTTATGTGAACATGCGCTGTGTGCTGCTTGCTT  
 TGGAAACT

FIG. 69B

Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser Arg Val Ser  
 Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln Ala Val Ser Trp Ala Ser  
 Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys Val Cys  
 Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr  
 Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly  
 Pro Ile Gln Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln  
 Lys Phe Gln Lys Val Lys Gly Phe Gly Ala Met Thr Asp Ala Ala Ala Leu  
 Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser  
 Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe Ser  
 Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser  
 Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu  
 Ala Gln Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys  
 Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile  
 Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu  
 His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu  
 Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln Arg Asp  
 Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg  
 Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val  
 Leu Thr Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu  
 Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro  
 Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser  
 Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile Thr Asn  
 Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu  
 Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr  
 Lys Asp Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys  
 Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu  
 Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn  
 Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu Glu  
 Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg Gln

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FIG. 70A

ATGGATGCAATGAAGAGAGGGGCTCTGCTGTGTGCTGCTGTGTGTTG  
AGCAGTCTTCGTTTCGCCCAGCCAGGAAATCCATGCCCGATTTCAGAA  
GAGGAGCCAGATCTTACCAAGTGATCTGCAGAGATGAAAAACGCA  
GATGATATACCAGCAACATCAGTCATGGCTGCGCCCTGTGCTCAGAA  
GCAACCGGGTGGAAATATTGCTGGTGCAACAGTGGCAGGGCAGAGTGC  
CACTCAGTGCCTGTCAAAAAGTTGCAGCGAGCCAAGGTGTTTCAACGG  
GGGCACCTGCCAGCAGGGCCCTGTACTTCTCAGATTTCGTGTGCCAGTG  
CCCCGAAGGATTTGCTGGGAAGTGCTGTGAAATAGATACCAGGGCCA  
CGTGCTACGAGGACCAGGGCATCAGCTACAGGGGGCACGTGGAGCAC  
AGCGGAGAGTGGCGCCGAGTGCACCAACTGGAACAGCAGCGCGTTG  
GCCCAGAAGCCCTACAGCGGGCGGAGGCCAGACGCCATCAGGCTGG  
GCCTGGGGAACCAACTACTGCAGAAACCCAGATCGAGACTCAAA  
GCCCTGGTGCTACGTCTTTAAGCGGGGAAGTACAGCTCAGAGTTCT  
GCAGCACCCCTGCCTGCTCTGAGGGAAACAGTGACTGCTACTTTGGG  
AATGGGTCAGCCTACCGTGGCACGCACAGCCTCACCGAGTCGGGTGC  
CTCCTGCCTCCCGTGGAAATTCATGATCCTGATAGGCAAGGTTTACAC  
AGCACAGAACCCCAAGTGGCCAGGCACTGGGCCCTGGGC AAAACATAATT  
ACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTG  
AAGAACCGCAGGCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTC  
CACCTGCGGCCCTGAGACAGTACAGCCAGCCTCAGTTTCGCATCAAAG  
GAGGGCTCTTTCGCCGACATCGCCTCCCAACCCCTGGCAGGCTGCCATCT  
TTGCCAAGCAGCAGGAGGTGCGCCGGGAGAGCGGTTCTGTGCGGGGGC  
ATACTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAG  
GAGAGGTTTCCGCCCCACCACTGACGGTGATCTTGGGCAGAACATA  
CCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAA  
TACATTGTCCATAAGGAATTCGATGACACTTACGACAATGACAT  
TGCGCTGCTGCAGCTGAAATCGGATTTCGTCCCGCTGTGCCCAGGAGA  
GCAGCGTGGTCCGCACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTG  
CCGGACTGGACGGAGTGTGAGCTCTCCGGCTACGGCAAGCATGAGGC  
CTTGCTCTCTTCTATTTCGGAGCGGCTGAAGGAGGCTCATGTACAGCT  
GTACCCATCCAGCCGCTGCACATCACAAACATTTACTTAACAGAAAC  
TCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGGCGGGCCC  
CAGGCAAACTTGACGACGCCTGCCAGGGCGATTCCGGGAGGCCCCCT  
GGTGTGTCTGAACGATGGCCGCATGACTTTGGTGGGCATCATCAGCT  
GGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACCAAG  
GTTACCAACTACCTAGACTGGATTTCGTGACAAACATGACACCGTGACC  
AGGAACACCCGACTCCTCAAAAGCAAATGAGATCC

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FIG. 70B

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly Ala Val  
Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg Gly Ala Arg Ser Tyr  
Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln Gln His Gln Ser Trp  
Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly  
Arg Ala Gln Cys His Ser Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn  
Gly Gly Thr Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro  
Glu Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu  
Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu Cys  
Thr Asn Trp Asn Ser Ser-Ala Leu Ala Gln Lys Pro Tyr Ser Gly Arg Arg Pro Asp  
Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys Arg Asn Pro Asp Arg Asp  
Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser  
Thr Pro Ala Cys Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr  
Arg Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met  
Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu Gly Leu  
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys Pro Trp Cys His  
Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys Asp Val Pro Ser Cys Ser  
Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe  
Ala Asp Ile Ala Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser  
Pro Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser  
Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile Leu Gly  
Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Gln Lys Phe Glu Val Glu Lys  
Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr Asp Asn Asp Ile Ala Leu  
Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg  
Thr Val Cys Leu Pro Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu  
Leu Ser Gly Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys  
Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn  
Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly Gly Pro  
Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys  
Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly  
Gln Lys Asp Val Pro Gly Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg  
Asp Asn Met Arg Pro

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FIG. 71A

ATCACTCTCTTAACTCACTACTCACATTAACCTCAACTCCTGCCACAA  
TGTAACAGGATGCAACTCCTGTCTTGCAATTGCACTAATTCTTGCACTTG  
TCACAAACAGTGCACCTACTTCAAGTTCGACAAAAGAAAACAAAAGAAA  
ACACAGCTACAACCTGGAGCATTACTGCTGGATTTACAGATGATTTTG  
AATGGAATTAATAATTACAAGAATCCCAAACTCACCAGGATGCTCAC  
ATTTAAGTTTTACATGCCCAAGAAGGCCACAGAACTGAAACAGCTTC  
AGTGTCTAGAAGAAGAACTCAAACCTCTGGAGGAAGTGCTGAATTTA  
GCTCAAAGCAAAAACCTTCACTTAAGACCCAGGGACTTAATCAGCAA  
TATCAACGTAATAGTTCTGGAACATAAGGGATCTGAAACAACATTCA  
TGTGTGAATATGCAGATGAGACAGCAACCATTGTAGAATTTCTGAAC  
AGATGGATTACCTTTTGTCAAAGCATCATCTCAACACTAACTTGATAA  
TTAAGTGCTTCCCACTTAAACATATCAGGCCTTCTATTTATTTATTTA  
AATATTTAAATTTTATATTTATTGTTGAATGTATGGTTGCTACCTATTG  
TAACTATTATTCTTAATCTTAAACTATAAATATGGATCTTTTATGAT  
TCTTTTTGTAAAGCCCTAGGGGCTCTAAAATGGTTTACCTTATTTATCC  
CAAAAATATTTATTTATTTATGTTGAATGTTAAATATAGTATCTATGTAG  
ATTGGTTAGTAAACTATTTAATAAAATTTGATAAATATAAAAAAAAAA  
AAACAAAAAAAAAAAA

FIG. 71B

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ile Leu Ala Leu Val Thr Asn  
Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Lys Lys Thr Gln Leu Gln Leu Glu  
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn  
Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr  
Glu Leu Lys Gln Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val  
Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser  
Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu  
Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys  
Gln Ser Ile Ile Ser Thr Leu Thr

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FIG. 72A-1

ATGCAAAATAGAGCTCTCCACCTGCTCTTTCTGTGCTTTTGTGCGATTCT  
GCTTTAGTGCCACCAGAAAGATACTACCTGGGTGCAGTGGAAGTGTCA  
TGGGACTATATGCAAAGTGATCTCGGTGAGCTGCCTGTGGACGCAAG  
ATTTCTCCTAGAGTGC AAAATCTTTCCATTCAACACCTCAGTCGT  
GTACAAAAAGACTCTGTTGTAGAATTCACGGATCACCTTTTCAACAT  
CGCTAAGCCCAAGGCCACCTGGATGGGTCTGCTAGGTCTACCATCC  
AGGCTGAGGTTTATGATACAGTGGTCATTACACTTAAGAACATGGCT  
TCCCATCCTGTGAGTCTTCATGCTGTTGGTGTATCCTACTGGAAGCT  
TCTGAGGGAGCTGAATATGATGATCAGACCAGTCAAAGGGAGAAAG  
AAGATGATAAAGTCTTCCCTGGTGAAGCCATACATATGTCTGGCAG  
GTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGCCTTAC  
CTACTCATATCTTTCTCATGTGGACCTGGTAAAAGACTTGAATTCAGG  
CCTCATTTGGAGCCCTACTAGTATGTAGAGAAGGGAGTCTGGCCAAGG  
AAAAGACACAGACCTTGCACAAAATTTATACTACTTTTGTCTGTATTTG  
ATGAAGGGAAAAAGTTGGCACTCAGAAACAAAGAACTCCTTGATCA  
GGATAGGGATGCTGCATCTGCTCGGGCCTGGCCTAAAATGCACACAG  
TCAATGGTTATGTAAACAGGTCTCTGCCAGGTCTGATTGGATGCCACA  
GGAAATCAGTCTATTGGCATGTGATTGGAATGGGCACCACTCTGAA  
GTGCACTCAATATTCTCGAAGGTACACATTTCTGTGAGGAACCAT  
CGCCAGGCGTCTTGGAAAATCTCGCCAATAACTTTCTTACTGCTCAA  
ACACTCTTGATGGACCTTGGACAGTTCTACTGTTTGTGCATATCTCTT  
CCCACCAACATGATGGCATGGAAGCTTATGTCAAAGTAGACAGCTGT  
CCAGGGAACCCCACTACGAATGAAAAATAATGAAGAAGCGGAAG  
ACTATGATGATGATCTTACTGATTCTGAAATGGATGCTGGTCAAGTTTG  
ATGATGACAACTCTCCTTCTTATCCAAATTCGCTCAGTTGCCAAGA  
AGCATCCTAAAACCTTGGGTACATTACATTGCTGCTGAAGAGGAGGAC  
TGGGACTATGCTCCCTTAGTCTCGCCCCGATGACAGAAGTTATAAA  
AGTCAATATTTGAACAAATGGCCCTCAGCGGATTGGTAGGAAGTACAA  
AAAAGTCCGATTTATGGCATACACAGATGAAACCTTTAAGACTCGTG  
AAGCTATTTCAGCATGAATCAGGAATCTTGGGACCTTTACTTTATGGGG  
AAGTTGGAGACACACTGTTGATTATTTAAGAATCAAGCAAGCAGA  
CCATATAACATCTACCCTCACGGAATCACTGATTCGCTCTTTGTAT  
TCAAGGAGATTACCAAAAGGTGTAAAAACATTTGAAGGATTTTCCAAT  
TCTGCCAGGAGAAATATTCAAATATAAATGGACAGTGAAGTGTAGAAG  
ATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTA  
GTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTC  
TCCTCATCTGTACAAAAGAATCTGTAGATCAAAGAGGAAACCGATA  
ATGTCAGACAAGAGGAATGTCATCCTGTTTCTGTATTTGATGAGAAC  
CGAAGCTGGTACCTCACAGAGAATATACAACGCTTCTCCCCAATCCA  
GCTGGAGTGCAGTTGAGGATCCAGAGTTCCAAGCCTCCAACATCAT  
GCACAGATCAAGTGGCTATGTTTTGATAGTTTGAGTTGTGAGTTTG  
TTTGCATGAGGTGGCATACTGGTACATTCTAAGCATTTGGAGACAGA  
CTGACTTCCTTTCTGTCTCTTCTCTGGATATACCTTCAAACACAAAAT

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FIG. 72A-2

GGTCTATGAAGACACACTCACCTATTCCCATTCTCAGGAGAAACTGT  
CTTCATGTGCGATGGAAAACCCAGGTCTATGGATTCTGGGGTGCCACA  
ACTCAGACTTTCCGAACAGAGGCATGACCGCCTTACTGAAGGTTTCT  
AGTTGTGACAAGAACACTGGTGATTATTACGAGGACAGTTATGAAGA  
TATTTTCAGCATACTTGTCTGAGTAAAAACAATGCCATTGAACCAAGAA  
GCTTCTCCCAGAATTCAAGACACCGTAGCACTAGGCCAAAAAGCAATTT  
AATGCCACCACAATTCCAGAAAAATGACATAGAGAAGACTGACCCCTG  
GTTTGACACAGAACACCTATGCCTAAAAATACAAAAATGTCTCCTCTA  
GTGATTGTGTGATGCTCTTGGCAGAGTGCTACTCCACATGGGCTAT  
CCTTATCTGTATCTCCAAGAAGCCAAATATGAGACTTTTTCTGATGATC  
CATCACCTGGAGCAATAGACAGTAATAACAGCCTGTCTGAAATGACA  
CACTTCAGGCCACAGCTCCATCAGTGGGGACATGGTATTTACCCC  
TGAGTCAGGCCTCCAATTAAGATTAAATGAGAACTGGGGACAACTG  
CAGCAACAGAGTTGAAGAAACTTGATTTCAAAGTTTCTAGTACATCA  
AATAATCTGATTTCAACAATTCCATCAGACAATTTGGCAGCAGGTACT  
GATAATACAAGTTTCCTTAGGACCCCCAAGTATGCCAGTTCATTATGAT  
AGTCAATTAGATACCACTCTATTTTGGCAAAAAAGTCATCTCCCCTTACT  
GAGTCTGGTGGACCTCTGAGCTTGAGTGAAGAAAAATGATTTCAAA  
GTTGTTAGAATCAGGTTTAATGAATAGCCAAGAAAGTTCATGGGGAA  
AAAAATGTATCGTCAACAGAGAGTGGTAGGTTATTTAAAGGGAAAAAGA  
GCTCATGGACCTGCTTTGTTGACTAAAGATAATGCCTTATTCAAAAGTT  
AGCATCTCTTTGTTAAAGACAAACAAAACCTTCCAATAATTCAGCAACT  
AATAGAAAGACTCAGCATTGATGGCCCATCTATTATAATGAGAATAG  
TCCATCAGTCTGGCAAAATATATTAGAAAGTGACACTGAGTTTAAAAA  
AAGTGACACCTTTGATTTCATGACAGAATGCTTATGGACAAAAATGCT  
ACAGCTTTGAGGCTAAATCATATGTCAAATAAAACTACTTCATCAAAA  
AAACATGGAAATGGTCCAACAGAAAAAGAGGGCCCCATCCACCA  
GATGCACAAAATCCAGATATGTCGTTCTTTAAGATGCTATTCTTGCCA  
GAATCAGCAAGGTGGATACAAAGGACTCATGGAAAGAACTCTCTGAA  
CTCTGGGCAAGGCCCCAGTCCAAAGCAATTAGTATCCTTAGGACCAG  
AAAAATCTGTGGAAGGTCAGAATTTCTGTCTGAGAAAAACAAAGTG  
GTAGTAGGAAAGGGTGAATTTACAAAGGACGTAGGACTCAAAGAGA  
TGTTTTTTCCAAGCAGCAGAAACCTATTCTTACTAAGTTGGATAATT  
TACATGAAAAATAATACACACAATCAAGAAAAAATAATTCAGGAAGA  
AATAGAAAAAGAAGGAAACATTAATCCAAGAGAATGTAGTTTTGCCTC  
AGATACATACAGTGACTGGCAGTAAAGAAATTCATGAAGAACCTTTTC  
TTACTGAGCACTAGGCAAAATGTAGAAGGTTTCATATGACGGGGCATA  
TGCTCCAGTACTTCAAGATTTTAGGTCATTAATGATTCAACAAATAG  
AACAAAGAAACACACAGCTCATTTCTCAAAAAAAGGGGAGGAAGAA  
AAGTTGGAAGGCTGGGAAATCAAACAGCAAATGTAGAGAAATAT  
GCATGCACCACAAGGAATATCTCCTAATACAAGCCAGCAGAAATTTG  
TCACGCAACGTAGTAAGAGAGCTTTGAAACAATTCAGACTCCCACTA

FIG. 72A-3

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GAAGAAACAGAACTTGAAAAAAGGATAATTGTGGATGACACCTCAAC  
CCAGTGGTCCAAAAACATGAAACATTTGACCCCGAGCACCCCTCACAC  
AGATAGACTACAATGAGAAGGAGAAAGGGGCCATTACTCAGTCTCCC  
TTATCAGATTGCCTTACGAGGAGTCATAGCATCCCTCAAGCAAAATAGA  
TCTCCATTACCCATTGCAAAGGTATCATTTCCATCTATTAGACCTA  
TATATCTGACCAGGGTCTATTCCAAGACAACCTTCTCATCTTCCAG  
CAGCATCTTATAGAAAAGAAAGATTCTGGGGTCCAAGAAAGCAGTCAT  
TTCTTACAAGGAGCCAAAAAAATAACCTTTCTTTAGCCATTCTAACC  
TTGGAGATGACTGGTGATCAAAGAGAGGTTGGCTCCCTGGGGACAAG  
TGCCACAAATTCAGTCACATACAAGAAAGTTGAGAACAACATGTTCTCCC  
GAAACCAGACTTGCCCCAAACATCTGGCAAAGTTGAATTGCTTCCAA  
AAGTTCACATTTATCAGAAGGACCTATTCCTACGGAAACTAGCAATG  
GGTCTCCTGGCCATCTGGATCTCGTGGAAGGGAGCCTTCTTCAGGGAA  
CAGAGGGAGCGATTAAGTGAATGAAGCAAACAGCCTGGAAAAAGT  
TCCCTTTCTGAGAGTAGCAACAGAAAGCTCTGCAAGAGACTCCCTCAA  
GCTATTGGATCCTCTTGCTTGGGATAACCACTATGGTACTCAGATACC  
AAAAGAAGAGTGGAAAATCCCAAGAGAAAGTCACCAGAAAAAACAGCT  
TTTAAGAAAAAGGATACCATTTTGTCCCTGAACGCTTGTGAAAAGCAAT  
CATGCAATAGCAGCAATAAAATGAGGGACAAAAATAAGCCGAAATAG  
AAGTCACCTGGGCAAAGCAAGGTAGGACTGAAAGGCTGTGCTCTCAA  
AACCCACCAGTCTTGAAACGCCATCAACGGGAAAATAACTCGTACTAC  
TCTTCAGTCAGATCAAGAGGAAATTGACTATGATGATACCATATCAGT  
TGAAATGAAGAAGGAAGATTTTGACATTTATGATGAGGATGAAAAT  
AGAGCCCCCGCAGCTTTCAAAAAGAAAACACGACACTATTTTATTGCTG  
CAGTGGAGAGGCTCTGGGATTATGGGATGAGTAGCTCCCCACATGTT  
CTAAGAAACAGGGCTCAGAGTGGCAGTGTCCCTCAGTTCAGAAAGT  
TGTTTTCCAGGAATTTACTGATGGCTCCTTTACTCAGCCCTTATACCGT  
GGAGAACTCAAAATGAACATTTGGGACTCCTGGGGCCATATATAAGAGC  
AGAAAGTTGAAGATAATATCATGGTAACTTTCAGAAATCAGGCCTCTC  
GTCCCTATTCTTCTATTCTAGCCTTATTTCTTATGAGGAAGATCAGAG  
GCAAGGAGCAGAACCTAGAAAAAATTTGTCAAGCCTAATGAAACCA  
AACTCTATTTTGGAAAAGTGCAACATCATATGGCAACCCACTAAAGAT  
GAGTTTGACTGCAAAGCCTGGGCTTATTTCTCTGATGTTGACCTGGAA  
AAAGATGTGCACTCAGGCCTGATTGGACCCCTTCTGGTCTGCCACACT  
AACACACTGAACCTGCTCATGGGAGACAAGTGACAGTACAGGAATT  
TGCTCTGTTTTTACCATCTTTGATGAGACAAAAGCTGGTACTTCACT  
GAAAAATATGGAAGAAACTGCAGGGCTCCCTGCAATATCCAGATGGA  
AGATCCCACTTTTAAAGAGAATTATCGCTTCCATGCAATCAATGGCTA  
CATAATGGATACACTACCTGGCTTAGTAATGGCTCAGGATCAAAGGA  
TTCGATGGTATCTGCTCAGCATGGGCAGCAATGAAAAACATCCATTCT  
ATTCAATTCAGTTGGACATGTGTTCACTGTACGAAAAAAAGAGAGTA  
TAAATGGCACTGTACAATCTCTATCCAGGTGTTTTTGGAGACAGTGA



FIG. 72A-4

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AATGTTACCATCCAAAGCTGGAATTTGGCGGGTGGAATGCCTTATTGG  
CGAGCATCTACATGCTGGGATGAGCACACTTTTCTGGTGTACAGCAA  
TAAGTGTACAGACTCCCCTGGGAATGGCTTCTGGACACATTAGAGATT  
TCAGATTACAGCTTCAGGACAATATGGACAGTGGGCCCCAAAGCTGG  
CCAGACTTCATTATTCCGGATCAATCAATGCTGGAGACCAAGGAG  
CCCTTTTCTTGATCAAGGTGGATCTGTTGGCACCAATGATTATTAC  
GGCATCAAGACCCAGGGTGCCCGTCAGAAGTTCTCCAGCCTCTACAT  
CTCTCAGTTTATCATCATGTATAGTCTTGATGGGAAGAAGTGGCAGA  
CTTATCGAGGAAATCCACTGGAACCTTAATGGTCTTCTTTGGCAATG  
TGGATTCATCTGGGATAAAAAACAATATTTTAAACCCTCCAATTATTG  
CTCGATACATCCGTTTGACCCAACTCATTATAGCATTTCGACGACTC  
TTCGCATGGAGTTGATGGGCTGTGATTAAATAGTTGCAGCATGCCAT  
TGGGAATGGAGAGTAAAGCAATATCAGATGCACAGATTACTGCTTCA  
TCCACTTTTACCAATATGTTTGCCACCTGGTCTCCTTCAAAGCTCGA  
CTTCACCTCCAAGGGAGGAGTAATGCCTGGAGACCTCAGGTGAATAA  
TCCAAAAGAGTGGCTGCAAGTGGACTTCCAGAAGACAATGAAAGTCA  
CAGGAGTAACTACTCAGGGAGTAAAATCTCTGCTTACCAGCATGTAT  
GTGAAGGAGTTCCCTCATCTCCAGCAGTCAAGATGGCCATCAGTGGAC  
TCTCTTTTTCAGAAATGGCAAAGTAAAGGTTTTTCAGGGAAATCAAGA  
CTCCTTCACACCTGTGGTGAACCTCTAGACCCACCCTTACTGACTCG  
CTACCTTCGAATTCACCCCCAGAGTTGGGTGCACCAGATTGCCCTGAG  
GATGGAGGTTCTGGGCTGCGAGGCACAGGACCTCTACTGAGGGTGGC  
CACTGCAGCACCTGCCACTGCCGTCACCTCTCCCTCCTCAGTCCAGG  
GCAGTGTCCCTCCCTGGCTTGCCCTTCTACCTTTGTGCTAAATCCTAGC  
AGACACTGCCTTGAAAGCCTCCTGAATTAACATATCATCAGTCTGCATT  
TCTTTGGTGGGGGCCAGGAGGGTGCATCCAATTTAACTTAACTCTTA  
CCTATTTTCTGCAGCTGTCTCCAGATTACTCTTCTTCCAATATAACT  
AGGCAAAAAGAAGTGAGGAGAAAACCTGCATGAAAGCATTCTTCCCTG  
AAAAGTTAGGCCTCTCAGAGTCACCACTTCTCTGTGTAGAAAACT  
ATGTGATGAACTTTGAAAAAGATATTTATGATGTTAACATTCAGGT  
TAAGCCTCATACGTTTAAAAATAAACTCTCAGTTGTTTATTATCCTGA  
TCAAGCATGGAACAAGAAGCATGTTTCAGGATCAGATCAATACAATCTT  
GGAGTCAAAAAGGCAAAATCATTTGGACAATCTGCAAAATGGAGAGAA  
TACAATAACTACTACAGTAAAGTCTGTTTCTGCTTCTTACACATAGA  
TATAATTATGTTATTTAGTCATTATGAGGGGCACATTCTTATCTCCAA  
AACTGACATTCCTTAAACTGAGAATTATAGATGGGGTCAAGAATCCC  
TAAGTCCCCTGAAATTATATAAGGCATTCTGTATAAATGCAAAATGTGC  
ATTTTTCTGACGAGTGTCCATAGATATAAAGCCATTTGGTCTTAATTCT  
GACCAATAAAAAAATAAGTCAGGAGGATGCAATTGTTGAAAGCTTTG  
AAATAAAATAACAATGTCTTCTTGAAATTTGTGATGGCCAAGAAAGA  
AAATGATGA

FIG. 72B-1

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Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe Cys Phe Ser  
Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr Met Gln Ser  
Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro Arg Val Pro Lys Ser Phe  
Pro Phe Asn Thr Ser Val Val Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His  
Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile  
Gln Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro  
Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Leu Gly Ala Glu Tyr  
Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val Phe Pro Gly Gly  
Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn Gly Pro Met Ala Ser Asp Pro  
Leu Cys Leu Thr Tyr Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn  
Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys  
Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser  
Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser Ala Arg  
Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu  
Ile Gly Cys His Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro  
Glu Val His Ser Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln  
Ala Ser Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp  
Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met Glu  
Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg Met Lys Asn  
Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val  
Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys  
Lys His Pro Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr  
Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn  
Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr  
Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile Leu Gly Pro  
Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser  
Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg  
Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile  
Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg  
Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala Ser  
Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn  
Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg  
Ser Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln  
Leu Glu Asp Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val  
Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu  
Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys  
His Lys Met Val Tyr Glu Asp Thr Leu Phe Pro Phe Ser Gly Glu Thr Val  
Phe Met Ser Met Glu Asn Pro Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe

FIG. 72B-2

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Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr  
 Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn  
 Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Arg Ser Thr Arg Gln  
 Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp Ile Glu Lys Thr Asp Pro Trp  
 Phe Ala His Arg Thr Pro Met Pro Lys Ile Gln Asn Val Ser Ser Ser Asp Leu Leu  
 Met Leu Leu Arg Gln Ser Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu  
 Ala Lys Tyr Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn  
 Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly Asp Met Val  
 Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu Lys Leu Gly Thr Thr  
 Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys Val Ser Ser Thr Ser Asn Asn Leu  
 Ile Ser Thr Ile Pro Ser Asp Asn Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu  
 Gly Pro Pro Ser Met Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly  
 Lys Lys Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu Asn  
 Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu Ser Ser Trp Gly  
 Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe Lys Gly Lys Arg Ala His Gly  
 Pro Ala Leu Leu Thr Lys Asp Asn Ala Leu Phe Lys Val Ser Ile Ser Leu Leu  
 Lys Thr Asn Lys Thr Ser Asn Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp  
 Gly Pro Ser Leu Leu Ile Glu Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu Ser  
 Asp Thr Glu Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg Met Leu Met Asp  
 Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met Ser Asn Lys Thr Thr Ser Ser  
 Lys Asn Met Glu Met Val Gln Gln Lys Lys Glu Gly Pro Ile Pro Pro Asp Ala  
 Gln Asn Pro Asp Met Ser Phe Phe Lys Met Leu Phe Leu Pro Glu Ser Ala Arg  
 Trp Ile Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro Ser Pro  
 Lys Gln Leu Val Ser Leu Gly Pro Glu Lys Ser Val Glu Gly Gln Asn Phe Leu  
 Ser Glu Lys Asn Lys Val Val Val Gly Lys Gly Glu Phe Thr Lys Asp Val Gly  
 Leu Lys Glu Met Val Phe Pro Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp  
 Asn Leu His Glu Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu Ile  
 Glu Lys Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile His Thr  
 Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu Leu Ser Thr Arg Gln  
 Asn Val Glu Gly Ser Tyr Asp Gly Ala Tyr Ala Pro Val Leu Gln Asp Phe Arg  
 Ser Leu Asn Asp Ser Thr Asn Arg Thr Lys Lys His Thr Ala His Phe Ser Lys  
 Lys Gly Glu Glu Glu Asn Leu Glu Gly Leu Gly Asn Gln Thr Lys Gln Ile Val  
 Glu Lys Tyr Ala Cys Thr Thr Arg Ile Ser Pro Asn Thr Ser Gln Gln Asn Phe  
 Val Thr Gln Arg Ser Lys Arg Ala Leu Lys Gln Phe Arg Leu Pro Leu Glu Glu  
 Thr Glu Leu Glu Lys Arg Ile Ile Val Asp Asp Thr Ser Thr Gln Trp Ser Lys Asn  
 Met Lys His Leu Thr Pro Ser Thr Leu Thr Gln Ile Asp Tyr Asn Glu Lys Glu  
 Lys Gly Ala Ile Thr Gln Ser Pro Leu Ser Asp Cys Leu Thr Arg Ser His Ser Ile  
 Pro Gln Ala Asn Arg Ser Pro Leu Pro Ile Ala Lys Val Ser Ser Phe Pro Ser Ile  
 Arg Pro Ile Tyr Leu Thr Arg Val Leu Phe Gln Asp Asn Ser Ser His Leu Pro

## FIG. 72B-3 304/498

Ala Ala Ser Tyr Arg Lys Lys Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu  
 Gln Gly Ala Lys Lys Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr  
 Gly Asp Gln Arg Glu Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser Val Thr  
 Tyr Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp Leu Pro Lys Thr Ser  
 Gly Lys Val Glu Leu Leu Pro Lys Val His Ile Tyr Gln Lys Asp Leu Phe Pro  
 Thr Glu Thr Ser Asn Gly Ser Pro Gly His Leu Asp Leu Val Glu Gly Ser Leu  
 Leu Gln Gly Thr Glu Gly Ala Ile Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys  
 Val Pro Phe Leu Arg Val Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser Lys Leu  
 Leu Asp Pro Leu Ala Trp Asp Asn His Tyr Gly Thr Gln Ile Pro Lys Glu Glu  
 Trp Lys Ser Gln Glu Lys Ser Pro Glu Lys Thr Ala Phe Lys Lys Lys Asp Thr Ile  
 Leu Ser Leu Asn Ala Cys Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly  
 Gln Asn Lys Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr Glu Arg  
 Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg His Gln Arg Glu Ile Thr Arg  
 Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu  
 Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg  
 Ser Phe Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp  
 Tyr Gly Met Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser Val  
 Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr Gln Pro  
 Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly Pro Tyr Ile Arg  
 Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro  
 Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu  
 Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val  
 Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr  
 Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu  
 Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln  
 Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu  
 Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr  
 Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro  
 Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly  
 Ser Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys  
 Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr  
 Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile Gly Glu  
 His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr  
 Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln  
 Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala  
 Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile  
 Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser  
 Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr Tyr Arg Gly  
 Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn Val Asp Ser Ser Gly Ile

FIG. 72B-4

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Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr  
His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn  
Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr  
Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu  
His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu  
Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln  
Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser  
Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe  
Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu  
Leu Thr Arg Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg  
Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr

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FIG. 73A

TCCACCTGTCCCCGAGCGCCGGCTCGCGCCCTCCTGCCGCAGCCACC  
GAGCCGCCGTCTAGCGCCCCGACCTCGCCACCATGAGAGCCCTGCTG  
GCGCGCCTGCTTCTCTGCGTCCTGGTCGTGAGCGACTCCAAAGGCAGC  
AATGAACTTCATCAAGTTCCATCGAACTGTGACTGTCTAAATGGAGGA  
ACATGTGTGTCCAACAAGTACTTCTCCAACATTCACTGGTGCAACTGC  
CCAAAGAAATTCGGAGGGCAGCACTGTGAAATAGATAAGTCAAAAAC  
CTGCTATGAGGGGAATGGTCACTTTTACCGAGGAAAGGCCAGCACTG  
ACACCATGGGCGGGCCCTGCCTGCCCTGGAACCTCTGCCACTGTCTTTC  
AGCAAACGTACCATGCCCACAGATCTGATGCTCTTCAGCTGGGCCTGG  
GGAAACATAATTACTGCAGGAACCCAGACAACCGGAGGCGACCCCTGG  
TGCTATGTGCAGGTGGGCCTAAAGCCGCTTGTTCCAAGAGTGATGGT  
GCATGACTGCGCAGATGGAAAAAAGCCCTCCTCTCCTCCAGAAGAAT  
TAAAATTTCAGTGTGGCCAAAAGACTCTGAGGCCCGCTTTAAGATTA  
TTGGGGGAGAATTCACCACCATCGAGAACCAGCCCTGGTTTGC GGCC  
ATCTACAGGAGGCACCGGGGGGGCTCTGTACCTACGTGTGTGGAGG  
CAGCCTCATCAGCCCTTGCTGGGTGATCAGCGCCACACACTGCTTCAT  
TGATTACCCAAAGAAGGAGGACTACATCGTCTACCTGGGTGCTCAA  
GGCTTAACCTCCAACACGCAAGGGGAGATGAAGTTTGAGGTGGA AAAAC  
CTCATCCTACACAAGGACTACAGCGCTGACACGCTTGCTCACCACAAC  
GACATTGCCTTGCTGAAGATCCGTTCCAAGGAGGGCAGGTGTGCGCA  
GCCATCCCGGACTATACAGACCATCTGCCTGCCCTCGATGTATAACGA  
TCCCCAGTTTGGCACAAGCTGTGAGATCACTGGCTTTGGAAAAGAGA  
ATTCTACCGACTATCTCTATCCGGAGCAGCTGAAGATGACTGTTGTGA  
AGCTGATTTCCCACCGGAGTGTCAGCAGCCCCACTACTACGGCTCTG  
AAGTACCCAGGAGGAAAATGCTGTGTGCTGACCCACAGTCAGTGAAACGA  
GATTCCTGCCAGGGAGACTCAGGGGGACCCCTCGTCTGTTCCCTCCAA  
GGCCGCATGACTTTGACTGGAATTGTGAGCTGGGGCCGTGGATGTGC  
CCTGAAGGACAAGCCAGGCGTCTACACGAGAGTCTCACACTTCTTAC  
CCTGGATCCGCAGTCACACCAAGGAAGAGAATGGCCTGGCCCTCTGA  
GGGTCCCCAGGGAGGAAAACGGGCACCAACCCGCTTTCTTGCTGGTTGTC  
ATTTTTGCAGTAGAGTCATCTCCATCAGCTGTAAGAAGAGACTGGGA  
AGAT

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FIG. 73B

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser Asp Ser  
Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly  
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn Cys Pro Lys  
Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn  
Gly His Phe Tyr Arg Gly Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro  
Trp Asn Ser Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu  
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg  
Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val His  
Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys  
Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile  
Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr  
Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys  
Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu  
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys  
Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg  
Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro  
Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys  
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys  
Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr Thr  
Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp  
Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val  
Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser  
His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu

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FIG.74A

TCCTGCACAGGCAGTGCCTTGAAGTGCTTCTTCAGAGACCTTTCTTCA  
TAGACTACTTTTTTTTCTTTAAGCAGCAAAAGGAGAAAAATTGTCATCA  
AGGATATTCCAGATTCTTGACAGCATTCTCGTCATCTCTGAGGACATC  
ACCATCATCTCAGGATGAGGGGCATGAAGCTGCTGGGGGCGCTGCTG  
GCACTGGCGGCCCTACTGCAGGGGGCCGTGTCCCTGAAGATCGCAGC  
CTTCAACATCCAGACATTTGGGGAGACCAAGATGTCCAATGCCACCCT  
CGTCAGCTACATTGTGCAGATCCTGAGCCGCTATGACATCGCCCTGGT  
CCAGGAGGTCAGAGACAGCCACCTGACTGCCGTGGGGAAGCTGCTGG  
ACAACCTCAATCAGGATGCACCAGACACCTATCACTACGTGGTCAGT  
GAGCCACTGGGACGGAACAGCTATAAGGAGCGCTACCTGTTTCGTGTA  
CAGGCCTGACCAGGTGTCTGCGGTGGACAGCTACTACTACGATGATG  
GCTGCGAGCCCTGCGGGAACGACACCTTCAACCGAGAGCCAGCCATT  
GTCAGGTTCTTCTCCCGTTTACAGAGGTCAGGGAGTTTGCCATTGTT  
CCCCTGCATGCGGCCCGGGGACGCAGTAGCCGAGATCGACGCTCT  
CTATGACGTCTACCTGGATGTCCAAGAGAAATGGGGCTTGGAGGACG  
TCATGTTGATGGGCGACTTCAATGCGGGCTGCAGCTATGTGAGACCCT  
CCCAGTGGTATCCATCCGCCTGTGGACAAGCCCCACCTTCCAGTGGC  
TGATCCCCGACAGCGCTGACACCACAGCTACACCCACGCACTGTGCCT  
ATGACAGGATCGTGGTTGCAGGGATGCTGCTCCGAGGCGCCGTTGTTC  
CCGACTCGGCTCTTCCCTTTAACTTCCAGGCTGCCTATGGCCTGAGTG  
ACCAACTGGCCCAAGCCATCAGTGACCACTATCCAGTGGAGGTGATG  
CTGAAGTGAGCAGCCCCCTCCCCACACCAGTTGAACTGCAG



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FIG. 74B

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu Leu Gln  
Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys  
Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp Ile  
Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val Gly Lys Leu Leu  
Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro  
Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln  
Val Ser Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn  
Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val  
Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile  
Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu Glu Asp  
Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln  
Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser  
Ala Asp Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly  
Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln  
Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val  
Glu Val Met Leu Lys

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FIG. 75A

GCTGCATCAGAAGAGGCCATCAAGCACATCACTGTCCTTCTGCCATGG  
CCCTGTGGATGCGCCTCCTGCCCTGCTGGCGCTGCTGGCCCTCTGGG  
GACCTGACCCAGCCGCAGCCTTTGTGAACCAACACCTGTGCGGCTCAC  
ACCTGGTGGAAGCTCTCTACCTAGTGTGCGGGGAACGAGGCTTCTTCT  
ACACACCCAAGACCCGCCGGGAGGCAGAGGACCTGCAGGTGGGGCA  
GGTGGAGCTGGGCGGGGGCCCTGGTGCAGGCAGCCTGCAGCCCTTGG  
CCCTGGAGGGGTCCCTGCAGAAGCGTGGCATTGTGGAACAATGCTGT  
ACCAGCATCTGCTCCCTCTACCAGCTGGAGAACTACTGCAACTAGACG  
CAGCCCGCAGGCAGCCCCCACCCGCCCTCCTGCACCGAGAGAGA  
TGAATAAAGCCCTTGAACCAGC

FIG. 75B

Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu Trp Gly  
Pro Asp Pro Ala Ala Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val  
Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr  
Arg Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly Pro  
Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile  
Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn

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FIG. 76A

ATGGGAGGTTGGTCTTCCAAACCTCGACAAGGCATGGGGACGAATCT  
TTCTGTTCCCAATCTCTGGGATTCTTTCCCGATCACCAGTTGGACCCT  
GCGTTCGGAGCCAACTCAAACAATCCAGATTGGGACTTCAACCCCAA  
CAAGGATCACTGGCCAGAGGCAATCAAGGTAGGAGCGGGAGACTTC  
GGGCCAGGGTTCACCCACCACACGGCGGTCTTTGGGGTGGAGCCC  
TCAGGCTCAGGGCATATTGACAACAGTGCCAGCAGCGCCTCCTCTG  
TTTCCACCAATCGGCAGTCAGGAAGACAGCCTACTCCCATCTCTCCAC  
CTCTAAGAGACAGTCATCCTCAGGCCATGCAGTGGAATCCACAACA  
TTCCACCAAGCTCTGCTAGATCCCAGAGTGAGGGGCCTATATTTCTCT  
GCTGGTGGCTCCAGTTCCGGAACAGTAAACCCGTGTTCCGACTACTGTC  
TCACCCATATCGTCAATCTTCTCGAGGACTGGGGACCCTGCACCGAAC  
ATGGAGAGCACAACATCAGGATTCTAGGACCCTGCTCGTGTACA  
GGCGGGGTTTTCTTGTTGACAAGAATCCTCACAATACCACAGAGTCT  
AGACTCGTGGTGGACTTCTCTCAATTTCTAGGGGGAGCACCCACGTG  
TCCTGGCCAAAATTGCGAGTCCCCAACCTCCAATCACTACCAACCTC  
TTGTCTCCAATTTGTCTGGTTATCGCTGGATGTGTCTCGCGCGTTTT  
ATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTGTGGTTC  
TTCTGGACTACCAAGGTATGTTGCCCGTTTGTCTCTACTTCCAGGAA  
CATCAACTACCAGCACGGGACCATGCAAGACCTGCACGATTCTGCT  
CAAGGAACCTCTATGTTCCCTCTTGTGCTGTACAAAACCTTCGGAC  
GGAAACTGCACCTGTATTCCCATCCCATCATCCTGGGCTTTCGCAAGA  
TTCTATGGGAGTGGGCCTCAGTCCGTTTCTCCTGGCTCAGTTTACTA  
GTGCCATTTGTGTCAGTGGTTCGACGGGCTTCCCCCACTGTTTGGCTTT  
CAGTTATATGGATGATGTGGTATTGGGGGCCAAGTCTGTACAACATCT  
TGAGTCCCTTTTACCTCTATTACCAATTTCTTTTGTCTTTGGGTATAC  
ATTTGA

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FIG. 76B

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu Ser Val Pro  
Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro Ala Phe Gly Ala Asn  
Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn Lys Asp His Trp Pro Glu Ala Ile  
Lys Val Gly Ala Gly Asp Phe Gly Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu  
Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro  
Val Ser Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu Arg  
Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu  
Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val  
Asn Pro Val Pro Thr Thr Val Ser Pro Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp  
Pro Ala Pro Asn Met Glu Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu  
Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser  
Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser  
Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr  
Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu  
Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu  
Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala  
Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn  
Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp  
Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Ala  
Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro  
Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu  
Trp Val Tyr Ile

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FIG. 77A

CGAACCCTCAGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCTA  
 CAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGC  
 CCTGGCTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGC  
 CTTTTGACAACGCTATGCTCCGCGCCCATCGTCTGCACCAGCTGGCCT  
 TTGACACCTACCAGGAGTTTGAAGAAGCCTATATCCCAAAGGAACAG  
 AAGTATTCATTCTGCAGAACCCCCAGACCTCCCTCTGTTTCTCAGAG  
 TCTATTCGACACCCCTCCAACAGGGAGGAAACACAACAGAAATCCAA  
 CCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGA  
 GCCCCTGCAGTTCCTCAGGAGTGTCTTCGCCAACAGCCTGGTGTACGG  
 CGCCTCTGACAGCAACGCTCTATGACCTCCTAAAGGACCTAGAGGAAG  
 GCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCGGACT  
 GGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACA  
 CAACGATGACGCTACTCAAGAACTACGGGCTGCTCTACTGCTTCAG  
 GAAGGACATGGCAAGGTCGAGACATTCCTGCGCATCGTGCAGTGCCG  
 CTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTG  
 TGACCCCTCCCAAGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGT  
 GCCCACCAGCCTGTCTAATAAAATTAAGTTGCATC

FIG. 77B

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu  
 Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu Ser Arg Pro Phe Asp  
 Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln  
 Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro  
 Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr  
 Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp  
 Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala  
 Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu  
 Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
 Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly  
 Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile  
 Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe

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FIG. 78A

ATGTATTCCAATGTGATAGGAACTGTAACCTCTGGAAAAAGGAAGGT  
TTATCTTTTGTCTTGTCTGCTCATTGGCTTCTGGGACTGCGTGACCTGT  
CACGGGAGCCCTGTGGACATCTGCACAGCCAAGCCGCGGGACATTCC  
CATGAATCCCATGTGCATTTACCGCTCCCCGGAGAAGAAGGCAACTG  
AGGATGAGGGCTCAGAACAGAAGATCCCGGAGGCCACCAACCGGCG  
TGCTGGGAACTGTCCAAGGCCAATTCCCGCTTTGCTACCACTTTCTA  
TCAGCACCTGGCAGATTCCAAGAATGACAATGATAACATTTTCCTGTCT  
ACCCCTGAGTATCTCCACGGCTTTTGTCTATGACCAAGCTGGGTGCTG  
TAATGACACCCTCCAGCAACTGATGGAGGTATTTAAGTTTGACACCAT  
ATCTGAGAAAAACATCTGATCAGATCCACTTCTTCTTTGCCAAACTGAA  
CTGCCGACTCTATCGAAAAAGCCAACAAATCCTCCAAGTTAGTATCAGC  
CAATCGCCTTTTTGGAGACAAATCCCTTACCTTCAATGAGACCTACCA  
GGACATCAGTGAGTTGGTATATGGAGCCAAGCTCCAGCCCCTGGACT  
TCAAGGAAAAATGCAGAGCAATCCAGAGCGGCCATCAACAAATGGGTG  
TCCAATAAGACCGAAGGCCGAATCACCGATGTCATTCCCTCGGAAGC  
CATCAATGAGCTCACTGTTCTGGTGCTGGTTAACACCATTACTTCAA  
GGGCTGTGGAAGTCAAAGTTCAGCCCTGAGAACACAAGGAAGGAAC  
TGTTCTACAAGGCTGATGGAGAGTCTGTTTCAGCATCTATGATGTACC  
AGGAAGGCAAGTTCCGTTATCGGCGCGTGGCTGAAGGCACCCAGGTG  
CTTGAGTTGCCCTTCAAAGGTGATGACATCACCATGGTCCTCATCTTG  
CCCAAGCCTGAGAAGAGCCTGGCCAAGGTGGAGAAGGAACTCACCCC  
AGAGGTGCTGCAGGAGTGGCTGGATGAATTGGAGGAGATGATGCTGG  
TGGTCCACATGCCCCGCTTCCGCATTGAGGACGGCTTCAGTTTGAAGG  
AGCAGCTGCAAGACATGGGCCTTGTGATCTGTTTCAGCCCTGAAAAA  
TCCAAATCCCAAGGTATTGTTGTCAGAAGGCCGAGATGACCTCTATGTC  
TCAGATGCATTCCATAAGGCATTTCTTGAGGTAAATGAAGAAGGCAG  
TGAAGCAGCTGCAAGTACCGCTGTTGTGATGCTGGCCGTTGCTATAA  
CCCCAACAGGGTGACTTTCAAGGCCAACAGGCCTTTCTGGTTTTAT  
AAGAGAAAGTTCCTCTGAACACTATTATCTTCATGGGCAGAGTAGCCA  
ACCTTGTGTTAAGTAA

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FIG. 78B

Met Tyr Ser Asn Val Ile Gly Thr Val Thr Ser Gly Lys Arg Lys Val Tyr Leu Leu  
Ser Leu Leu Leu Ile Gly Phe Trp Asp Cys Val Thr Cys His Gly Ser Pro Val Asp  
Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn Pro Met Cys Ile Tyr Arg Ser  
Pro Glu Lys Lys Ala Thr Glu Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr  
Asn Arg Arg Val Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr  
Gln His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser  
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr Leu Gln Gln  
Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys Thr Ser Asp Gln Ile His  
Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser  
Lys Leu Val Ser Ala Asn Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu  
Thr Tyr Gln Asp Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe  
Lys Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr  
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu Thr Val Leu  
Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys Ser Lys Phe Ser Pro Glu  
Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser  
Met Met Tyr Gln Glu Gly Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln  
Val Leu Glu Leu Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys  
Pro Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu  
Trp Leu Asp Glu Leu Glu Met Met Leu Val Val His Met Pro Arg Phe Arg  
Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met Gly Leu Val Asp  
Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile Val Ala Glu Gly Arg Asp Asp  
Leu Tyr Val Ser Asp Ala Phe His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser  
Glu Ala Ala Ala Ser Thr Ala Val Val Ile Ala Gly Arg Ser Leu Asn Pro Asn Arg  
Val Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn  
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys

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FIG. 79A

ATGGATTACTACAGAAAATATGCAGCTATCTTTCTGGTCACATTGTCG  
GTGTTTCTGCATGTTCTCCATTCCGCTCCTGATGTGCAGGATTGCCAG  
AATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCA  
ATACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCA  
CTAAGGTCCAAGAAGACGATGTTGGTCCAAAAGAACGTCACCTCAGA  
GTCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCACAGTAATGGG  
GGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTGTT  
ATTATCACAAATCTTAA

FIG. 79B

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser Val Phe Leu  
His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu  
Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe  
Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn  
Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met  
Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His  
Lys Ser



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FIG. 79C

ATGGAGATGTTCCAGGGGCTGCTGCTGTTGCTGCTGCTGAGCATGGGC  
GGGACATGGGCATCCAAGGAGCCGCTTCGGCCACGGTGCCGCCCCAT  
CAATGCCACCCTGGCTGTGGAGAAGGAGGGCTGCCCCGTGTGCATCA  
CCGTCAACACCACCATCTGTGCCGGCTACTGCCCCACCATGACCCGCG  
TGCTGCAGGGGGTCCTGCCGGCCCTGCCTCAGGTGGTGTGCAACTACC  
GCGATGTGCGCTTCGAGTCCATCCGGCTCCCTGGCTGCCCGCGCGGCG  
TGAACCCCGTGGTCTCCTACGCCGTGGCTCTCAGCTGTCAATGTGCAC  
TCTGCCGCCGAGCACCCTGACTGCGGGGGTCCCAAGGACCACCCC  
TTGACCTGTGATGACCCCGCTTCCAGGACTCCTCTCCTCAAAGGCC  
CCTCCCCCAGCCTTCCAAGCCCATCCCGACTCCCGGGGCCCTCGGAC  
ACCCCGATCCTCC CACAATAA

FIG. 79D

Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly Gly Thr  
Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala  
Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala Gly  
Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val  
Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg  
Gly Val Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu Cys  
Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp  
Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser  
Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln

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FIG. 80A

ATGCGTCCCCTGCGCCCCCGCGCCGCGTGTGCGGCTCCTGGCCTCG  
CTCCTGGCCGCGCCCCCGGTGGCCCCGCGCGAGGCCCGCACCTGGT  
GCAGGTGGACGCGGCCCGCGCGCTGTGGCCCCCTGCGGCGCTTCTGGA  
GGAGCACAGGCTTCTGCCCCCGCTGCCACACAGCAGGCTGACCAG  
TACGTCCTCAGCTGGGACCAGCAGCTCAACCTCGCCTATGTGGGCGCC  
GTCCCTCACCGCGGCATCAAGCAGGTCCGGACCCACTGGCTGCTGGA  
GCTTGTCACCAACAGGGGGTCCACTGGACGGGGCCTGAGCTACAACT  
TCACCCACCTGGACGGGTACTTGGACCTTCTCAGGGAGAACCAGCTCC  
TCCCAGGGTTTGAGCTGATGGGCAGCGCCTCGGGCCACTTCACTGACT  
TTGAGGACAAGCAGCAGGTGTTTTGAGTGGAAGGACTTGGTCTCCAGC  
CTGGCCAGGAGATACATCGGTAGGTACGGACTGGCGCATGTTTCAA  
GTGGAACCTTCGAGACGTGGAATGAGCCAGACCACCACTTTGACA  
ACGTCTCCATGACCATGCAAGGCTTCTGAACTACTACGATGCCTGCT  
CGGAGGGTCTGCGCGCCGCCAGCCCCGCTGCGGCTGGGAGGCCCC  
GGCGACTCCTTCCACACCCACCGCGATCCCCGCTGAGCTGGGGCCTC  
CTGCGCCACTGCCACGACGGTACCAACTTCTTCACTGGGGAGGCGGG  
CGTGCGGCTGGACTACATCTCCCTCCACAGGAAGGGTGCGCGCAGCT  
CCATCTCCATCCTGGAGCAGGAGAAGGTGCTCGCGCAGAGTGGCGG  
CAGCTCTTCCCCAAGTTCGCGGACACCCCCATTTACAACGACGAGGCG  
GACCCGCTGGTGGGCTGGTCCCTGCCACAGCCGTGGAGGGCGGACGT  
GACCTACGCGGCCATGGTGGTGAAGGTCACTCGCGCAGCATCAGAACC  
TGCTACTGGCCAAACCACTCCGCTTCCCCTTCCGCTCCTGAGCA  
ACGACAATGCCTTCTGAGCTACCACCCGACCCCTTCGCGCAGCGCA  
CGCTCACCGCGCGCTTCCAGGTCAACAACACCCGCCCGCCGACGTG  
CAGCTGTTGCGCAAGCCGGTGCTCACGGCCATGGGGCTGCTGGCGCT  
GCTGGATGAGGACGAGCTCTGGGCCGAAGTGTCGACGGCCGGGACCG  
TCCTGGACAGCAACCACACGGTGGGCGTCTGGCCAGCGCCACCGC  
CCCCAGGGCCCGGCCGACGCTGGCGCGCCGCGGTGCTGATCTACGC  
GAGCGACGACACCCGCGCCACCCCAACCGCAGCGTTCGCGGTGACCC  
TGCGGCTGCGCGGGTGCCCCCGGGCCGGGCTGGTCTACGTCACG  
CGCTACCTGGACAACGGGCTCTGCAGCCCCGACGGCGAGTGCGCGG  
CCTGGGCGGCGCCGCTTCCCCACGGCAGAGCAGTTCGGGCGCATGC  
GCGCGGCTGAGGACCCGGTGGCCGCGGGCGCCCGCCCTTACCCGCC  
GGCGGCCGCTGACCTGCGCCCCGCGCTGCGGCTGCCGTGCTTTTG  
CTGGTCAAGTGTGTGCGCGCCCGAGAAGCCGGGAGGTAC  
GCGGCTCCGCGCCCTGCCCTGACCCAAGGGCAGCTGGTTCTGGTCTG  
GTCGGATGAACACGTGGGCTCCAAGTGCCTGTGGACATACGAGATCC  
AGTTCTCTCAGGACGGTAAGGCGTACACCCGGTCAGCAGGAAGCCA  
TCGACCTTCAACCTTTGTGTTTACGCCAGACACAGGTGCTGTCTCT  
GGCTCCTACCGAGTTCGAGCCCTGGACTACTGGGCCGACCAAGCC  
CTTCTCGGACCCTGTGCCGTACCTGGAGGTCCCTGTGCCAAGAGGGCC  
CCCATCCCCGGGCAATCCATGA

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FIG. 80B

Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser Leu Leu  
 Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val Gln Val Asp Ala Ala  
 Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg Ser Thr Gly Phe Cys Pro Pro Leu  
 Pro His Ser Gln Ala Asp Gln Tyr Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala  
 Tyr Val Gly Ala Val Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu  
 Glu Leu Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr His  
 Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro Gly Phe Glu  
 Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu Asp Lys Gln Gln Val  
 Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala Arg Arg Tyr Ile Gly Arg Tyr Gly  
 Leu Ala His Val Ser Lys Trp Asn Phe Glu Thr Trp Asn Glu Pro Asp His His Asp  
 Phe Asp Asn Val Ser Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys  
 Ser Glu Gly Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser  
 Phe His Thr Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His Cys His Asp  
 Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu Asp Tyr Ile Ser Leu His  
 Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile Leu Glu Gln Glu Lys Val Val Ala Gln  
 Gln Ile Arg Gln Leu Phe Pro Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala  
 Asp Pro Leu Val Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala  
 Ala Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn Thr Thr  
 Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe Leu Ser Tyr His Pro  
 His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg Phe Gln Val Asn Asn Thr Arg  
 Pro Pro His Val Gln Leu Leu Arg Lys Pro Val Leu Thr Ala Met Gly Leu Leu Ala  
 Leu Leu Asp Glu Glu Gln Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu  
 Asp Ser Asn His Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala  
 Asp Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala His Pro  
 Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro Pro Gly Pro Gly Leu  
 Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu Cys Ser Pro Asp Gly Glu Trp  
 Arg Arg Leu Gly Arg Pro Val Phe Pro Thr Ala Glu Gln Phe Arg Arg Met Arg  
 Ala Ala Glu Asp Pro Val Ala Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu  
 Thr Leu Arg Pro Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala  
 Arg Pro Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln  
 Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys Leu Trp Thr  
 Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr Thr Pro Val Ser Arg Lys Pro  
 Ser Thr Phe Asn Leu Phe Val Phe Ser Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr  
 Arg Val Arg Ala Leu Asp Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro  
 Tyr Leu Glu Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro

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FIG. 81A

ATGCAGCTGAGGAACCCAGAACTACATCTGGGCTGCGCGCTTGCCT  
TCGCTTCCTGGCCCTCGTTTCCTGGGACATCCCTGGGGCTAGAGCACT  
GGACAATGGATTGGCAAGGACGCCTACCATGGGCTGGCTGCACTGGG  
AGCGCTTCATGTGCAACCTTGACTGCCAGGAAGAGCCAGATTCTGC  
ATCAGTGAGAAGCTCTTCATGGAGATGGCAGAGCTCATGGTCTCAGA  
AGGCTGGAAGGATGCAGGTTATGAGTACCTCTGCATTGATGACTGTTG  
GATGGCTCCCCAAAGAGATTGAGAAGGCAGACTTCAGGCAGACCCTC  
AGCGCTTCCTCATGGGATTGCCAGCTAGCTAATTATGTTACAGCA  
AAGGACTGAAGCTAGGGATTTATGCAGATGTTGGAAATAAAACCTGC  
GCAGGCTTCCCTGGGAGTTTGGATACTACGACATTGATGCCAGACC  
TTTGCTGACTGGGGAGTAGATCTGCTAAAATTTGATGGTTGTTACTGT  
GACAGTTTGAAAAATTTGGCAGATGGTTATAAGCACATGTCCTTGGCC  
CTGAATAGGACTGGCAGAAGCATTGTGTACTCCTGTGAGTGGCCTCTT  
TATATGTGGCCCTTTCAAAAGCCCAATTATACAGAAATCCGACAGTAC  
TGCAATCACTGGCGAAATTTTGCTGACATTGATGATTCCTGGAAAAAGT  
ATAAAGAGTATCTTGGACTGGACATCTTTTAAACCAGGAGAGAATTGTT  
GATGTTGCTGGACCAGGGGGTTGGAATGACCCAGATATGTTAGTGAT  
TGGCAACTTTGGCCTCAGCTGGAATCAGCAAGTAACTCAGATGGCCCT  
CTGGGCTATCATGGCTGCTCCTTTATTCATGTCTAATGACCTCCGACA  
CATCAGCCCTCAAGCCAAAGCTCTCCTTCAGGATAAGGACGTAATTGC  
CATCAATCAGGACCCCTTGGGCAAGCAAGGGTACCAGCTTAGACAGG  
GAGACAACCTTTGAAGTGTGGGAACGACCTCTCTCAGGCTTAGCCTGG  
GCTGTAGCTATGATAAAACCGCAGGAGATTGGTGGACCTCGCTCTTAT  
ACCATCGCAGTTGCTTCCCTGGGTAAAGGAGTGGCCTGTAATCCTGCC  
TGCTTCATCACACAGCTCCTCCCTGTGAAAAGGAAGCTAGGGTCTAT  
GAATGGACTTCAAGGTTAAGAAGTCACATAAATCCACAGGCACTGT  
TTTGCTTCAGCTAGAAAATACAATGCAGATGTCATTAAGGACTTACT  
TTAA

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FIG. 81B

Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu Arg Phe  
Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu Asp Asn Gly Leu Ala  
Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg Phe Met Cys Asn Leu Asp  
Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser Glu Lys Leu Phe Met Glu Met Ala Glu  
Leu Met Val Ser Glu Gly Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp  
Cys Trp Met Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln  
Arg Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu Lys  
Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe Pro Gly Ser Phe  
Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp Trp Gly Val Asp Leu Leu Lys  
Phe Asp Gly Cys Tyr Cys Asp Ser Leu Glu Asn Leu Ala Asp Gly Tyr Lys His  
Met Ser Leu Ala Leu Asn Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro  
Leu Tyr Met Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn  
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser Ile Leu  
Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala Gly Pro Gly Gly Trp  
Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe Gly Leu Ser Trp Asn Gln Gln  
Val Thr Gln Met Ala Leu Trp Ala Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp  
Leu Arg His Ile Ser Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala  
Ile Asn Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn  
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala Met Ile Asn  
Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala Val Ala Ser Leu Gly Lys  
Gly Val Ala Cys Asn Pro Ala Cys Phe Ile Thr Gln Leu Leu Pro Val Lys Arg Lys  
Leu Gly Phe Tyr Glu Trp Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr  
Val Leu Leu Gln Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu

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FIG. 82A

ATGGCGCCCGTCGCCGTCTGGGCCGCGCTGGCCGTCGGACTGGAGCT  
CTGGGCTGCGGCGCACGCCTTGCCCGCCAGGTGGCATTACACCCTA  
CGCCCCGGAGCCCGGGAGCACATGCCGGCTCAGAGAATACTATGACC  
AGACAGCTCAGATGTGCTGCAGCAAATGCTCGCCGGGCCAACATGCA  
AAAGTCTTCTGTACCAAGACCTCGGACACCGTGTGTGACTCCTGTGAG  
GACAGCACATACCCCAGCTCTGGAACCTGGGTCCCCGAGTGCTTGAG  
CTGTGGCTCCCGCTGTAGCTCTGACCAGGTGGAACTCAAGCCTGCAC  
TCGGGAACAGAACCGCATCTGCACCTGCAGGCCCGGCTGGTACTGCG  
CGCTGAGCAAGCAGGAGGGGTGCCGGCTGTGCGCGCCGCTGCGCAAG  
TGCCGCCCCGGGCTTCGGCGTGGCCAGACCAGGAACCTGAAACATCAGA  
CGTGGTGTGCAAGCCCTGTGCCCCGGGGACGTTCTCCAACACGACTTC  
ATCCACGGATATTTCAGAGCCCCACCAGATCTGTAACGTGGTGGCCAT  
CCCTGGGAATGCAAGCATGGATGCAGTCTGCACGTCCACGTCCCCCA  
CCCGGAGTATGGCCCCAGGGGCAGTACACTTACCCACGCCAGTGTC  
ACACGATCCCAACACACGCAGCCAACTCCAGAACCCAGCACTGCTCC  
AAGCACCTCCTTCTGCTCCCAATGGGCCCCAGCCCCCAGCTGAAGG  
GAGCACTGGCGACTTCGCTCTTCCAGTTGGACTGATTGTGGGTGTGAC  
AGCCTTGGGTCTACTAATAATAGGAGTGGTGAACGTGTGCATCATGAC  
CCAGGTGAAAAAGAAGCCCTTGTGCCTGCAGAGAGAAGCCAAGGTGC  
CTCACTTGCCCTGCCGATAAGGCCCGGGGTACACAGGGCCCCGAGCAG  
CAGCACCTGCTGATCACAGCGCCGAGCTCCAGCAGCAGCTCCCTGGA  
GAGCTCGGCCAGTGCGTTGGACAGAAGGGCGCCACTCGGAACACAGC  
CACAGGCCACCAGGCGTGGAGGCCAGTGGGGCCGGGGAGGCCGGGC  
CAGCACCGGGAGCTCAGATTCTTCCCTGGTGGCCATGGGACCCAGG  
TCAATGTACCTGCATCGTGAACGTCTGTAGCAGCTCTGACCACAGCT  
CACAGTGTCTCTCCCAAGCCAGCTCCACAATGGGAGACACAGATTCC  
AGCCCCCTCGGAGTCCCCGAAGGACGAGCAGGTCCCTTCTCCAAGGA  
GGAATGTGCCTTTCGGTCACAGCTGGAGACGCCAGAGACCCTGCTGG  
GGAGCACCGAAGAGAAGCCCCCTGCCCTTGGAGTGCCTGATGCTGGG  
ATGAAGCCCAGTTAACCAGGCCGGTGTGGGCTGTGTCTGATGCCAAGG  
TGGGCTGAGCCCTGGCAGGATGACCTGCGAAGGGGCCCTGGTCTT  
CCAGGC

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FIG. 82B

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala  
Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser  
Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys  
Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys  
Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys  
Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg  
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln  
Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val  
Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr  
Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val  
Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr  
Arg Ser Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln  
His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro  
Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val Gly  
Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val Val Asn Cys Val  
Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro  
His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu  
Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Leu Asp Arg  
Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly  
Glu Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His Gly Thr Gln  
Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys  
Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro  
Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu  
Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro  
Asp Ala Gly Met Lys Pro Ser

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FIG. 83A

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val  
Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln  
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly  
Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser  
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro  
Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

FIG. 83B

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg  
Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg  
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr  
Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys  
Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr  
Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln  
Gly Thr Leu Val Thr Val Ser Ser



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FIG. 84A

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln Thr Leu Thr  
Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser Gly Met Ser Val Gly Trp  
Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu Trp Leu Ala Asp Ile Trp Trp Asp Asp  
Lys Lys Asp Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser  
Lys Asn Gln Val Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr  
Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala Gly  
Thr Thr Val Thr Val Ser Ser

FIG. 84B

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val  
Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met His Trp Tyr Gln Gln Lys  
Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val  
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser  
Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe  
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

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FIG. 85A

GACATCTTGCTGACTCAGTCTCCAGCCATCCTGTCTGTGAGTCCAGGA  
 GAAAGAGTCAGTTTCTCCTGCAGGGCCAGTCAGTTTCGTTGGCTCAAGC  
 ATCCACTGGTATCAGCAAAGAACAATGGTTCCTCAAGGCTTCTCATA  
 AAGTATGCTTCTGAGTCTATGTCTGGGATCCCTTCCAGGTTTAGTGGC  
 AGTGGATCAGGGACAGATTTTACTCTTAGCATCAACACTGTGGAGTCT  
 GAAGATATTGCAGATTATTACTGTCAACAAAGTCATAGCTGGCCATTC  
 ACGTTCGGCTCGGGGACAAATTTGGAAGTAAAAGAAGTGAAGCTTGA  
 GGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCT  
 CCTGTGTTGCCTCTGGATTCAATTTTCAGTAACCACTGGATGAACTGGG  
 TCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGA  
 TCAAAATCTATTAATTCTGCAACACATTATGCGGAGTCTGTGAAAGGG  
 AGGTTACCATCTCAAGAGATGATTCCAAAAGTGCTGTCTACCTGCAA  
 ATGACCGACTTAAGAACTGAAGACACTGGCGTTTATTACTGTTCCAGG  
 AATTACTACGGTAGTACCTACGACTACTGGGGCCAAGGCACCACTCTC  
 ACAGTCTCC

FIG. 85B

Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly Glu Arg Val  
 Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser Ile His Trp Tyr Gln Gln  
 Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser Met Ser Gly  
 Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn  
 Thr Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro  
 Phe Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu Glu Ser  
 Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser Cys Val Ala Ser Gly  
 Phe Ile Phe Ser Asn His Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu  
 Glu Trp Val Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu  
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr  
 Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg  
 Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser

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FIG. 86A

ATGGAGACAGACACACTCCTGTTATGGGTGCTGCTGCTCTGGGTTC  
GGTTCCTACTGGTGACGTCAAGGCGAGGGCCCCGGAGCCTGCGGGGCAG  
GGACGCGCCAGCCCCACGCCCTGCGTCCCGGCCGAGTGCTTCGACC  
TGCTGGTCCGCCACTGCGTGCCCTGCGGGCTCCTGCGCACGCCGCGGC  
CGAAACCGGCCGGGGCCAGCAGCCCTGCGCCCAGGACGGCGCTGCAG  
CCGCAGGAGTCGGTGGGCGCGGGGGCCGCGCAGGCGGCGGTGACACA  
AACTCACACATGCCCCACCGTGCCAGCACCTGAACTCCTGGGGGGA  
CCGTCAGTCTTCTCTTCCCCCAAAACCCAAAGGACACCCTCATGATC  
TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGACGTGAGCCACGA  
AGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGAGGTGC  
ATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTA  
CCGTGTGGTCAGCGTCCTCACCCTGTCACCAGGACTGGCTGAATGG  
CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCA  
TCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAG  
GTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGT  
CAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT  
GGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACG  
CCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTC  
ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTC  
CGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT  
CCCTGTCTCCCGGAAATGA

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FIG. 86B

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro Gly Ser  
Thr Gly Asp Val Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg Asp Ala Pro Ala  
Pro Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu Leu Val Arg His Cys Val Ala  
Cys Gly Leu Leu Arg Thr Pro Arg Pro Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro  
Arg Thr Ala Leu Gln Pro Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val  
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser  
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu  
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr  
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys  
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro  
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

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FIG. 87

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val  
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln  
Lys Pro Asp Gly Ile Val Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly  
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser  
Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro  
Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

FIG. 88

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Gly Pro Gly Thr Ser Val Arg  
Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Lys  
Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly  
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser  
Thr Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe  
Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Arg Gly Thr  
Leu Val Thr Val Ser Ala

FIG. 89

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val  
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln  
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly  
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser  
Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu  
Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys

FIG. 90

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys  
Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Arg  
Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly  
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser  
Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr  
Phe Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly  
Thr Leu Val Thr Val Ser Ser

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FIG. 91

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val  
 Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln  
 Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly  
 Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Thr Leu Thr Ile Ser  
 Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu  
 Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys Arg Thr Val Ala Ala Pro  
 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val  
 Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val  
 Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys  
 Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys  
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys  
 Ser Phe Asn Arg Gly Glu Cys

FIG. 92

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys  
 Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Arg  
 Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly  
 Thr Asn Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser  
 Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr  
 Phe Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly  
 Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala  
 Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp  
 Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val  
 His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val  
 Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
 Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His  
 Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe  
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu  
 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser  
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp  
 Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser  
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu  
 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly

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FIG. 93A

ATGGATTTCAGGTGCAGATTATCAGCTTCCTGCTAATCAGTGCTTCA  
GTCATAATGTCCAGAGGGCAAATIGTTCTCTCCAGTCTCCAGCAATC  
CTGTCTGCATCTCCAGGGGAGAAGGTCACAATGACTTGCCAGGGCCAG  
CTCAAGTGTAAGTTACATCCACTGGTTCCAGCAGAAGCCAGGATCCTC  
CCCCAAACCCTGGATTTATGCCACATCCAACCTGGCTTCTGGAGTCCC  
TGTTGCTTCAGTGCCAGTGGGTCTGGGACTTCTTACTCTCTCACAAT  
CAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGT  
GGACTAGTAACCCACCCACGTTCTGGAGGGGGGACCAAGCTGGAATC  
AAA

FIG. 93B

Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser Val Ile Met Ser  
Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly Glu  
Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile His Trp Phe Gln  
Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser  
Gly Val Pro Val Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn  
Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

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FIG. 94A

ATGGGTTGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTACGCGTG  
TCCTGTCCCAGGTACAACCTGCAGCAGCCTGGGGCTGAGCTGGTGAAG  
CCTGGGGCCTCAGTGAAGATGTCTGCAAGGCTTCTGGCTACACATT  
ACCAGTTACAATATGCACTGGGTAAAACAGACACCTGGTCGGGGCCT  
GGAATGGATTGGAGCTATTATCCCGGAAATGGTGATACTTCCTACAA  
TCAGAAAGTTCAAAGGCAAGGCCACATTGACTGCAGACAAATCCTCCA  
GCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCG  
GTCTATTACTGTGCAAGATCGACTTACTACGGCGGTGACTGGTACTTC  
AATGTCTGGGGCGCAGGGACCACGGTCACCGTCTCTGCA

FIG. 94B

Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg Val Leu Ser  
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys  
Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys  
Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp  
Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser  
Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr  
Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly Ala Gly  
Thr Thr Val Thr Val Ser Ala



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FIG. 95A

GACGTCGCGGCCGCTCTAGGCCTCCAAAAAGCCTCCTCACTACTTCT  
GGAATAGCTCAGAGGCCGAGGCGGCCTCGGCCTCTGCATAAAATAAAA  
AAAATTAGTCAGCCATGCATGGGCGGAGAATGGGCGGAACCTGGGCG  
GAGTTAGGGGCGGGATGGGCGGAGTTAGGGGCGGGACTATGGTTGCT  
GACTAATTGAGATGCATGCTTTGCATACTTCTGCCTGCTGGGAGCCT  
GGGGACTTTCCACACCTGGTTGCTGACTAATTGAGATGCATGCTTTGC  
ATACTTCTGCCTGCTGGGGAGCCTGGGGACTTTCCACACCCTAACTGA  
CACACATTCCACAGAATTAATTTCCCTAGTTATTAATAGTAATCAATT  
ACGGGTCATTAGTTCATAGCCCATATATGGAGTTCGCGTTACATAA  
CTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCGGCC  
ATTGACGTCATAATGACGTATGTTCCCATAGTAACGCCAATAGGGA  
CTTTCCATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCCACT  
TGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACG  
TCAATTGACGGTAAATGGCCCGCCTGGCATTATGCCAGTACATGACCT  
TATGGGACTTTTCTACTTGGCAGTACATCTACGTATTAGTACATCGTA  
TTACCATGGTGATGCGGTTTGGCAGTACATCAATGGGCGTGGATAGC  
GGTTTGACTACGGGGATTTCGAAGTCTCCACCCCATTTGACGTCAATG  
GGAGTTTGTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA  
ACAACCTCCGCCCATTTGACGCAAAATGGGCGGTAGCGGTGACGGTGG  
GAGGTCTATATAAGCAGAGCTGGGTACGTGAACCGTCAGATCGCCTG  
GAGACGCCATCACAGATCTCTCACCATGAGGGTCCCCGCTCAGCTCCT  
GGGGCTCCTGCTGCTCTGGCTCCCAGGTGCACGATGTGATGGTACCAA  
GGTGAAAATCAAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCC  
GCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCT  
GCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGG  
ATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAG  
GACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAG  
CAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAAGTCAACC  
ATCAGGGCCTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAG  
TGTTGAATTGAGATCCGTTAACGGTTACCAACTACCTAGACTGGATT  
GTGACAACATGCGGCGGTGATATCTACGTATGATCAGCCTCGACTGTG  
CCTTCTAGTTGCCAGCCATCTGTTGTTTGGCCCTCCCCGCTGCTTCC  
TGACCCTGGAAGGTGCCACTCCCCTGTCCTTTTCTAATAAAATGAGG  
AAATTGCATCGCATTTGTTCTGAGTAGGTGTCATTCTATTCTGGGGGGTG  
GGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAG  
GCATGCTGGGGATGCGGTGGGCTCTATGGAACCACTGGGGCTCGAC  
AGCTATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGC  
CCGCTTGGCATTATGCCAGTACATGACCTTATGGGACTTTCTACTT  
GGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGT  
TTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGA  
TTTCCAAGTCTCCACCCCATTTGACGTCAATGGGAGTTGTTTGGCAC

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FIG. 95B

CAAAATCAACGGGACTTTCCAAAATGTCGTAACAACCTCCGCCCCATTG  
ACGCAAATGGGCGGTAGGCGTGACGGTGGGAGGTCTATATAAGCAG  
AGCTGGGTACGTCCTCACATTACAGTGATCAGCACTGAACACAGACCC  
GTCGACATGGGTTGGAGCCTCATCTTGCTCTTCCTTGTGCGTGTGTGCTA  
CGCGTGTGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCT  
CCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTC  
AAGGACTACTTCCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGCGC  
CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCTCAGG  
ACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGG  
CACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCA  
AGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACCTCACACA  
TGCCACCGTGGCCAGCACCTGAACTCTGGGGGGACCGCTAGTCTTC  
CTCTTCCCCCAAAACCCAAAGGACACCCTCATGATCTCCCGGACCCCT  
GAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGT  
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA  
CAAAGCCGCGGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTCAGC  
GTCCTACCGTCTCTGCACCAGGACTGGCTGAATGGCAAGGACTACAA  
GTGCAAGGTCTCCAACAAGCCCTCCACGCCCTCCGAGAAAACCA  
TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG  
CCCCCATCCCGGGATGAGCTGACCAGGAACAGGTACGCCTGACCTG  
CCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGA  
GCAATGGGCAGCCGGGAGAAACAACACAGACAGCCCTCCCGTGTGCTG  
GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAG  
AGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGCATGA  
GGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG  
TAAATGAGGATCCGTTAACGGTTACCAACTACCTAGACTGGATTGCTG  
ACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTGCCT  
TCTAGTTGCCAGCCATCTGTTGTTGGCCCTCCCCCGTGCCTTCCTTGA  
CCCTGGAAGGTGCCACTCCCACTGTCTTCTCAATAAAATGAGGAAA  
TTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGG  
TGGGCGAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCA  
TGCTGGGGATGCGGTGGGCTCTATGGAACAGCTGGGGCTCGACAGC  
GCTGGATCTCCCGATCCCCAGCTTGTCTTCTCAATTCTTATTGTCATA  
ATGAGAAAAAAGGAAAAATTAATTTTAACACCAATTGAGTAGTTGAT  
TGAGCAAAATGCGTTGGCAAAAAGGATGCTTAGAGACAGTGTCTCT  
GCACAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAG  
ACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAAATATGCTT  
GTCATACCCGAAGCCTGATTCCGTAGAGCCACACCTTGTTAAGGGCC  
AATCTGCTACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCAT  
ATAAGGTGAGGTAGGATCAGTTGCTCCTCAATTTGCTTCTGACATAG  
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGG

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FIG. 95C

GCTGCGATTTCGCGCCAAACTTGACGGCAATCCTAGCGTGAAGGCTG  
GTAGGATTTTATCCCCGCTGCCATCATGGTTCGACCATTTGAAGTGCAT  
CGTCGCCGTGTCCAAAAATATGGGGATTGGCAAGAACGGAGACCTAC  
CCTGGCCCTCCGCTCAGGAACGAGTTCAAGTACTTCCAAAGAATGACC  
ACAACTCTTCAGTGGAAGGTAAACAGAATCTGGTGATTATGGGTAG  
GAAAACCTGGTTCTCCATTCTTGAGAACATCGACCTTTAAAGGACA  
GAATTAATATAGTTCTCAGTAGAGAAGTCAAAGAACCACCACGAGGA  
GCTCATTTTCTTGCCAAAAGTTTGGATGATGCCTTAAGACTTATTGAA  
CAACCGGAATTGGCAAGTAAAGTAGACATGGTTTGGATAGTCGGAGG  
CAGTTCTGTTTACCAGGAAGCCATGAATCAACCAGGCCACCTTAGACT  
CTTTGTGACAAGGATCATGCAGGAATTTGAAAAGTGACACGTTTTTCCC  
AGAAATTGATTTGGGGAAATATAAACTTCTCCAGAATACCCAGGCG  
TCCTCTCTGAGTCCAGGAGGAAAAAGGCATCAAGTTATAAGTTGAA  
GTCTACGAGAAGAAAGACTAACAGGAAGATGCTTCAAGTTCTCTGC  
TCCCCTCTAAAGTCATGCATTTTATAAGACCATGGGACTTTTGCTG  
GCTTTAGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTGT  
TTGCCCTCCCCCGTGCCTTCTTGACCTGGAAGGTGCCACTCCCAC  
TGTCTTTCTCTAATAAATGAGGAAATTCATCGCATTTGTCTGAGTAG  
GTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGG  
AGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCT  
ATGGAACCAAGCTGGGGCTCGAGCTACTAGCTTTGCTTCTCAATTTCTT  
ATTTGCATAATTGACAAAAAAGGAAAAATTAATTTAACACCAATTCA  
GTAGTTGATTGAGCAAAATGCGTTGCCAAAAAGGATGCTTTAGAGACA  
GTGTCTCTGCACAGATAAGGACAAACATTATTAGAGGGAGTACCC  
AGAGCTGAGACTCTAAGCCAGTGAGTGGCACAGCATTTAGGGAGA  
AATATGCTTGTCATCACCGAAGCCTGATTCGCTAGAGCCACACCTGG  
TAAGGGCCAATCTGCTCACACAGGATAGAGAGGCGAGGACCGGCT  
CAGAGCATATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTC  
TGACATAGTTGTGTTGGGAGCTTGGATCGATCCTCTATGGTTGAACAA  
GATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  
GGCTATGACTGGGACAAACAGACAATCGGCTGCTCTGATGCCGCCGT  
GTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGA  
CCTGTCCGGTGCCCTGAATGAAGTGCAGGACGAGGACGCGCGCTAT  
CGTGGCTGGCCACGACGGGCGTTCTTGGCGCAGCTGTGCTCGACGTTG  
TCACTGAAGCGGGACAGGACTGGCTGCTATTGGGCGAAGTGCCGGGG  
CAGGATCTCCTGTCTCTACCTTGCTCCTGCCGAGAAAGTATCCATC  
ATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGC  
CCATTGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCG  
GATGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGAGCATC  
AGGGGCTCGCGCCAGCCGAACCTGTTCCGAGGCTCAAGGCGCGCATG  
CCCACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTCCG

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FIG. 95D

AATATCATGGTGGAAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGC  
CGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCG  
TGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCGT  
GCTTTACGGTATCGCCGCTTCCGATTTCGACGCGCATCGCCTTCTATC  
GCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGAC  
CGACCAAGCGACGCCCCAACC TGCCATCAGGAGATTTGATTCCACCG  
CCGCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTCCGGGACGCCG  
GCTGGATGATCCTCCAGCGCGGGATCTCATGCTGGAGTTCTTCGCCC  
ACCCCAACTTGTTTATTGACGCTTATAATGGTTACAAATAAAGCAATA  
GCATCACAATTTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTT  
GTGGTTTGTCACAACTCATCAATCTATCTTATCATGTCTGGATCGCGG  
CCGCGATCCCGTCGAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCC  
TGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGG  
AGCATAAAGTGTAAGCCCTGGGGTGCCCTAATGAGTCGATTAACAC  
ATTAATTGCGTTGCGCTCACTGCCGCTTTCAGTCGGGAAACCTGTC  
GTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTT  
TGCGTATTGGGCGCTCTTCCGCTTCTCGCTCACTGACTCGCTGCGCTC  
GGTCGTTCCGGTTCGGCGGAGCGGTATCAGCTCACTCAAAGGCGGTAA  
TACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGA  
GCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCGTTGC  
TGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATC  
GACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATAC  
CAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCGTATCCGACC  
CTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTG  
GCGCTTCTCAATGTCTACGCTGTAGGTATCTCAGTTCGGTGTAGGTC  
GTTCTGCTTCAAGCTGGGCTGTGTACGAACCCCCGTTACGCCCCGAC  
CGCTGCGCCTTATCCGGTAACCTATCGTCTTGAGTCCAACCGGTAAGA  
CACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAG  
AGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTA  
ACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGA  
AGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTGATCCGGCAAA  
CAAACACCGCTGGTAGCGGTGGTTTTTTTTGTTTGCAGAACTGGATTT  
ACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTAC  
GGGCTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGG  
TCATGAGATTATCAAAAAAGGATCTTCACTAGATCCTTTTAAATTA  
AATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTG  
ACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTC  
TATTTCTGTTATCCATAGTTGCCTGACTCCCGTCGTGTAGATAACTAC  
GATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGC  
GAGACCCACGCTACCGCTCCAGATTTATCAGCAATAAACACGCCA  
GCCGGAAGGGCCGAGCGCAGAAGTGGTCTGCAACTTTATCCGCTC  
CATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCG

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FIG. 95E

CAGTTAATAGTTTGC GCAACGTTGTTGCCATTGCTACAGGCATCGTGG  
TGTCACGCTCGTCGTTTGGIATGGCTTCATTCAGCTCCGGTTCCCAAC  
GATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTT  
AGCTCCTTCGGTCCTCCGATCGTTGT CAGAAGTAAGTTGGCCGCAGTG  
TTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGC  
CATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCAT  
TCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAA  
TACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATC  
ATTGGAAAACGTTCTTCGGGGCGAAAAC TCTCAAGGATCTTACCGCTG  
TTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCA  
GCATCTTTTACTTTACCCAGCGTTTCTGGGTGAGCAAAAACAGGAAGG  
CAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAATGTTGAA  
TACTCATACTCTTCTTTTCAATATTATTGAAGCATTATCAGGGTTA  
TTGTCTCATGAGCGGATACATATTTGAATGTATTAGAAAAATAAAACA  
AATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCT

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FIG. 96A

GACGTCGCGGCCGCTCTAGGCCTCCAAAAAGCCTCCTCACTACTTCT  
GGAATAGCTCAGAGGCCGAGGCGGCCTCGGCCTCTGCATAAAATAAAA  
AAAATTAGTCAGCCATGCATGGGGCGGAGAATGGGCGGAACCTGGGCG  
GAGTTAGGGGCGGGATGGGCGGAGTTAGGGGCGGGACTATGGTTGCT  
GACTAATTGAGATGCATGCTTTGCATACTTCTGCCTGCTGGGGAGCCT  
GGGGACTTTCCACACCTGGTTGCTGACTAATTGAGATGCATGCTTTGC  
ATACTTCTGCCTGCTGGGGAGCCTGGGGACTTTCCACACCCTAAGTGA  
CACACATTCCACAGAAATTAATCCCTAGTTATTAATAGTAATCAATT  
ACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCGCGGTTACATAA  
CTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCC  
ATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGA  
CTTTCCATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCCACT  
TGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACG  
TCAATGACGGTAAATGGCCCGCCTGGCATTATGCCAGTACATGACCT  
TATGGGACTTTCTACTTGGCAGTACATCTACGTTATAGTCAATCGTGA  
TTACCATGGTGATGCGGTTTTTGGCAGTACATCAATGGGCGTGGATACC  
GGTTTGACTCACGCGGATTTCCAAGTCTCCACCCCATTGACGTCAATG  
GGAAGTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAAATGTCGTA  
ACAACCTCCGCCCATTTGACGCAAAATGGGCGGTAGCCGCAATAGGGA  
GAGGTCTATATAAGCAGAGCTGGGTACGTGAACCGTCAGATCGCCTG  
GAGACGCCATCACAGATCTCTCACTATGGATTTTCAGGTGCAGATTAT  
CAGCTTCTCTGTAATCAGTGCTTCAGTCATAATGTCCAGAGGACAAAT  
TGTTCTCTCCCACTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAA  
GGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAAGTTACATCCACT  
GGTTCCAGCAGAAGCCAGGATCCTCCCCCAAACCTGGATTTATGCCA  
CATCCAACCTGGCTTCTGGAGTCCCTGTTTCGCTTCAGTGGCAGTGGGT  
CTGGGACTTCTACTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATG  
CTGCCACTTATTACTGCCAGCAGTGGACTAGTAACCCACCCACGTCG  
GAGGGGGGACCAAGCTGGAAATCAAACGTACGGTGGCTGCACCATCT  
GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCC  
TCTGTTGTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTA  
CAGTGGAAGGTGGATAACGCCCTCCAATCGGTAAGTCCCAGGAGAG  
TGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCA  
CCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCC  
TGCGAAGTCAACCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTT  
CAACAGGGGAGAGTGTGAATTCAGATCCGTTACCGTTACCAACTA  
CCTAGACTGGATTCTGTGACAACATGCGGCCGTGATATCTACGTATGAT  
CAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGGCCCTC  
CCCCGTGCCTTCTTGACCTGGAAGGTGCCACTCCCACTGTCTTTCC

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FIG. 96B

TAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCT  
ATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGG  
AAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGAACCA  
GCTGGGGCTCGACGCTATGCCAAGTACGCCCCCTATTGACGTCAATG  
ACGGTAAATGGCCGCGCTGGCATTATGCCCAGTACATGACCTTATGGG  
ACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCAT  
GGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTTG  
ACTACGGGGATTTCCAAAGTCTCCACCCCATTGACGTCAATGGGAGTT  
TGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACT  
CCGCCCCATTGACGCAAAATGGGCGGTAGGCGTGTACGGTGGGAGGTC  
TATATAAGCAGAGCTGGGTACGTCTCACATTCAGTGATCAGCACTGA  
ACACAGACCCGTCGACATGGGTTGGAGCCTCATCTTGCTCTTCCTTGT  
CGCTGTTGTACGCGTGTCTGTCCAGGTACAACCTCAGCAGCAGCTGG  
GGCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATGTCCTGCAAGG  
CTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAACAGA  
CACCTGGTCGGGGCCTGGAATGGATTGGAGCTATTTATCCCGGAAAT  
GGTGATACCTTCTACAATCAGAAGTCAAAGGCAAGGCCACATTGAC  
TGCAGACAAATCCTCCAGCACAGCCTACATGCAAGCTCAGCAGCTGA  
CATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCGACTTACTACG  
GCGGTGACTGGTACTTCAATGTCTGGGGCGCAGGGACCACGGTCACC  
GTCTCTGCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC  
TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGT  
CAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAAGTCAAGCG  
CCCTGACCAGCGGCGTGCACACCTTCCCGGTGTCTTACAGTCTCTAG  
GACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGG  
GCACCCAGACCTACATCTGCAACGTGAATCAAGCCAGCAACACC  
AAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGCAAAAACCTCACAC  
ATGCCCCACCGTGCCAGCACCTGAACTCTGGGGGGACCGTCAGTCTT  
CCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCC  
TGAGGTCAATGCTGGTGGTGGTGGAGCTGAGCCACGAAGACCCCTGAGG  
TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGAGTATGCGCAAG  
ACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTTCAG  
CGTCTCACCGTCTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACA  
AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCC  
ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAGGTGTACACCCT  
GCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGACGCTGACCT  
GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAG  
AGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGTCT  
GGACTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAA  
GAGCAGGTGGCAGCAGGGGAACGCTTCTCATGTCTCCGTGATGCGATG  
AGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGG  
GTAAATGAGGATCCGTTAACGGTTACCAACTACCTAGACTGGATTCTGT

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FIG. 96C

GACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTGCC  
TTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCCCCGTGCCTTCCTTG  
ACCCCTGGAAGGTGCCACTCCCACTGTCTTTTCTTAATAAAATGAGGAA  
ATTGCAATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGGTGGG  
GTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGC  
ATGCTGGGGATGCGGTGGGCTCTATGGAACCACTGGGGCTCGACAG  
CGCTGGATCTCCCGATCCCCAGCTTTGCTTCTCAATTTCTTATTTCAT  
AATGAGAAAAAAGGAAAAATTAATTTTAACACCAATTCAGTAGTTGA  
TTGAGCAAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTCTCT  
GCACAGATAAAGGACAAACATTATTTCAGAGGGAGTACCCAGAGCTGAG  
ACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTT  
GTCAATCACCAGAGCCTGATTCCTGAGAGCCACACCTTGGTAAGGGCC  
AATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCAT  
ATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAG  
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGGGCTCGCATTCG  
CGCCAAACTTGACGGCAATCCTAGCGTGAAGGCTGGTAGGATTTTATC  
CCCGCTGCCATCATGGTTTCGACCATTTGAATGTCATCGTCGCGGTGTC  
CAAAATATGGGATTGGCAAGAACGGAGACCTACCCTGGCCCTCCGCT  
CAGGAACGAGTTCAGTACTTCCAAAGAATGACCACAACTCTTCAG  
TGGAAGGTAAACAGAATCTGGTGATTATGGGTAGGAAAACCTGGTTC  
TCCATTCTGAGAAGAAATCGACCTTTAAAGGACAGAATTAATATAGTT  
CTCAGTAGAGAACTCAAAGAACCACGAGGAGCTCATTTTCTTGC  
CAAAAGTTTGGATGATGCCCTTAAGACTTATGAAACCCGAATTGG  
CAAGTAAAGTAGACATGGTTTGGATAGTCGGAGGCAGTCTGTTTACC  
AGGAAGCCATGAATCAACCAGGCCACCTTAGACTCTTTGTGACAAGG  
ATCATGCAGGAATTTGAAAAGTGACACGTTTTTCCAGAAATTGATTG  
GGGAAATATAAACTTCTCCAGAATACCCAGGCGTCTCTGA  
GGTCCAGGAGGAAAAAGGCATCAAGTATAAGTTTGAAGTCTACGAGA  
AGAAAGACTAACAGGAAGATGCTTTCAAGTTCTCTGCTCCCCCTCTAA  
AGCTATGCATTTTATAAGACCATGGGACTTTTGCTGGCTTTAGATCA  
GCCTCGACTGTGCCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCC  
CCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACCTGCTTCTTA  
ATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTAT  
TCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAA  
GACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGAACCACT  
TGGGGCTCGAGCTACTAGCTTTGCTTCTCAATTTCTATTGTCATAATG  
AGAAAAAAGGAAAAATTAATTTTAACACCAATTCAGTAGTTGATTGA  
GCAAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTCTCTGCA  
CAGATAAGGACAAACATTATTTCAGAGGGAGTACCCAGAGCTGAGACT  
CCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTTGTG  
ATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCCAAT  
CTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCATATA  
AGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAGTTG



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FIG. 96D

TGTTGGGAGCTTGGATCGATCCTCTATGGTTGAACAAGATGGATTGCA  
CGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCCGGCTATGACTG  
GGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTC  
AGCGCAGGGGCGCCCGTTCTTTTGTCAAAGACCGACCTGTCCGGTGC  
CCTGAATGAACTGCAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCA  
CGACGGGCGTTCTTGCAGCTGTGCTCGACGTTGTCACTGAAGCGG  
GAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTG  
TCATCTCACCTTGCTCCTGCGGAGAAAGTATCCATCATGGCTGATGCA  
ATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCAC  
CAAGCGAAACATCGCATCGAGCGAGCACGTA CTGGATGGAAGCCGG  
TCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGC  
CAGCCGAAC TGTTCCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGAG  
GATCTCGTCGTGACCCATGGCGATGCCGTGCTTGCCGAATATCAGCCAC  
GAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTG  
GCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGA  
AGAGCTTGGCGGGCGAATGGGCTGACCGCTTCTCGTGCTTTACGGTAT  
CGCCGCTCCGATTCTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGA  
GTTCTTCTGAGCGGGACTCTGGGGTTTCGAAATGACCGACCAAGCGAC  
GCCAACCTGCCATCACGAGATTTTCGATTCCACCGCCGCTTCTATGA  
AAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCT  
CCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCCAACTTGTT  
TATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTT  
CACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTGTCCAA  
ACTCATCAATCTATCTTATCATGTCTGGATCGCGGCCGCGATCCCGTC  
GAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGTGTGAAATGTT  
TATCCGCTTACAAATTTCCACACAACATACGAGCCGGAAGCATAAAGTG  
TAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTT  
GCGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTCGTGCCAGCTGCA  
TTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGC  
GCTTCTCCGCTTCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCCGGCT  
GCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCA  
CAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCA  
GCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCC  
ATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGT  
CAGAGGTGGCGAAACCCGACAGGACTATAAAGATACACGGCTTCTCC  
CCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGCTTAC  
CGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCA  
ATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAA  
GCTGGGCTGTGTGCACGAACCCCGGTTACGCCGACCGCTGCGCCTT  
ATCCGGTAACATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATC

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FIG. 96E

GCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATG  
TAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTAC  
ACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACC  
TTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCCGC  
TGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAA  
AAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGC  
TCAGTGGAAACGAAAACCTCACCTAGATCCTTTAAATAAAAATGAAGTTTAA  
AAAAAGGATCTTCACCTAGATCCTTTAAATAAAAATGAAGTTTAA  
ATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATG  
CTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCC  
ATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGG  
CTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTC  
ACCGGCTCCAGATTTATCAGCAATAAACAGCCAGCCGGAAGGGCCG  
AGCGCAGAAGTGGTCTGCAACTTTATCCGCTCCATCCAGTCTATTA  
ATTGTTGCCGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGC  
GCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTACGCTCGTCGT  
TTGGTATGGCTTCATTAGCTCCGGTTCCCAACGATCAAGGCGAGTTA  
CATGATCCCCCATGTTGTGCAAAAAAGCGTTAGCTCCTTCGGTCTC  
CGATCGTTGTGAGAAGTAAGTTGGCCGAGTGTTATCACTCATGGTTA  
TGGCAGCACTGCATAATTTCTTACTGTGATGCCATCCGTAAGATGCT  
TTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTA  
TGCGGCGACCGAGTTGCTCTTGCCGCGGTCAATACGGGATAATACC  
GCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTCTC  
TCGGGGCGAAAACCTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTTCG  
ATGATACCCACTCGTGCACCAACTGATCTTCAGCATCTTTTACTTTCA  
CCAGCGTTTCTGGGTGAGCAAAAAACAGGAAGGCAAAATGCCGCAAAA  
AAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTCTCT  
TTTTCAATATTATTGAAGCATTATCAGGGTATTGTCTCATGACGG  
ATACATATTGAATGTATTTAGAAAAATAAACAAATAGGGGTCCGC  
GCACATTTCCCGAAAAAGTGCCACCT

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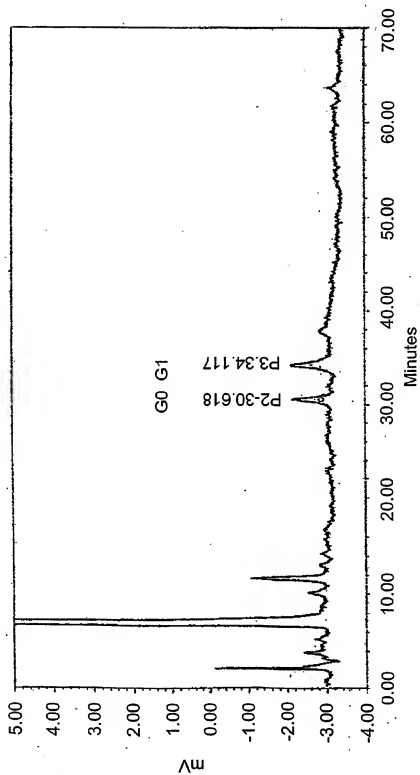


FIG. 97A

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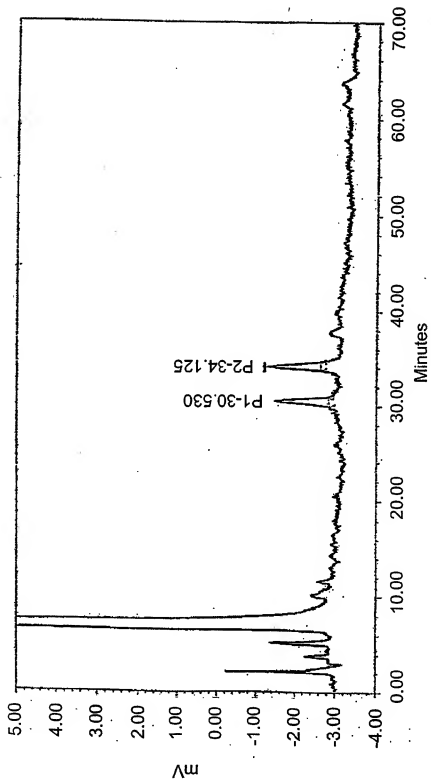


FIG. 97B

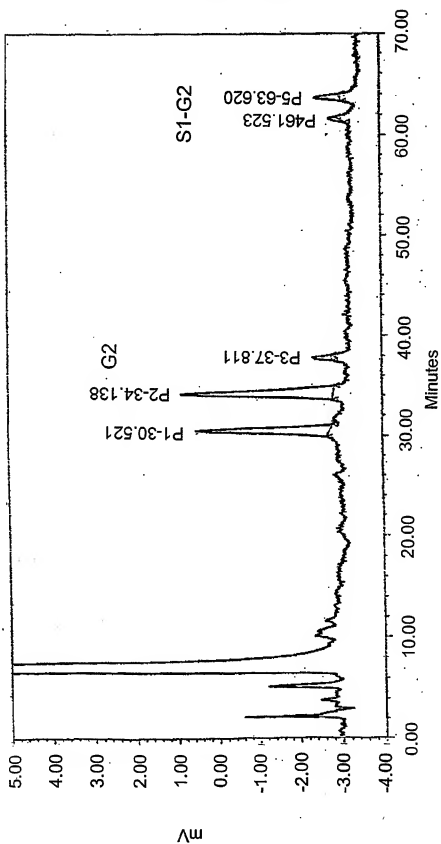


FIG. 97C

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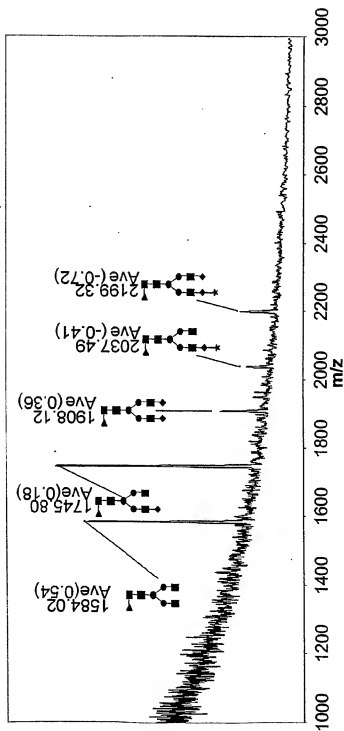


FIG. 98A

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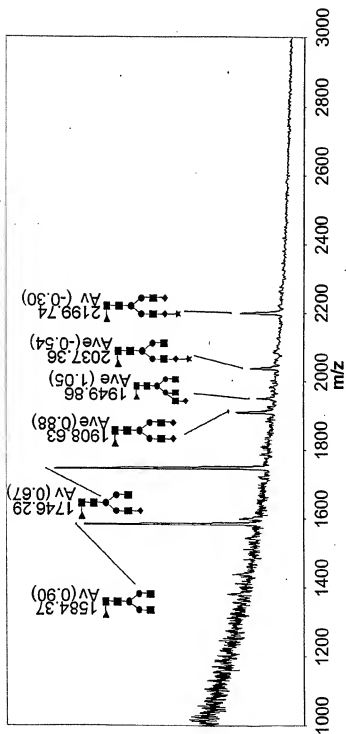


FIG. 98B

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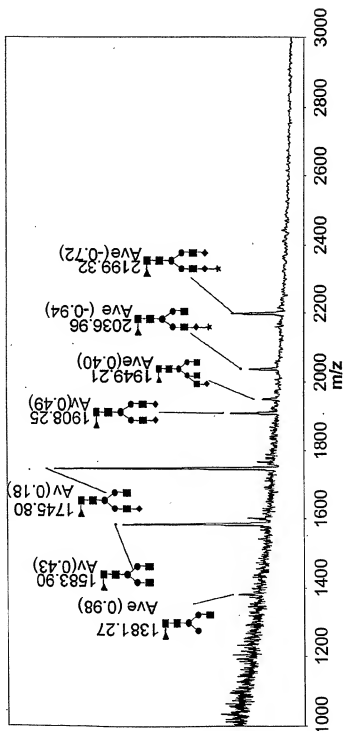


FIG. 98C



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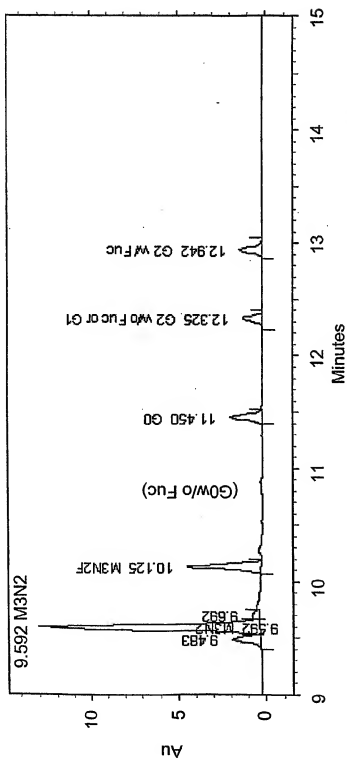


FIG. 99A

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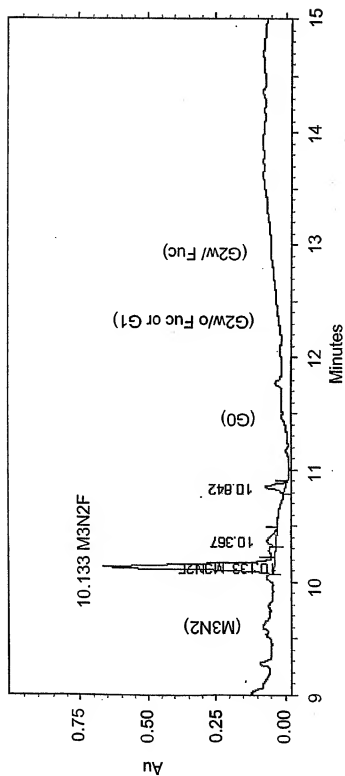


FIG. 99B

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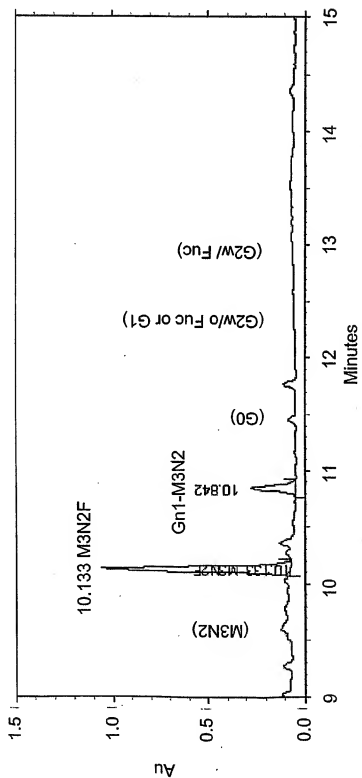


FIG. 99C

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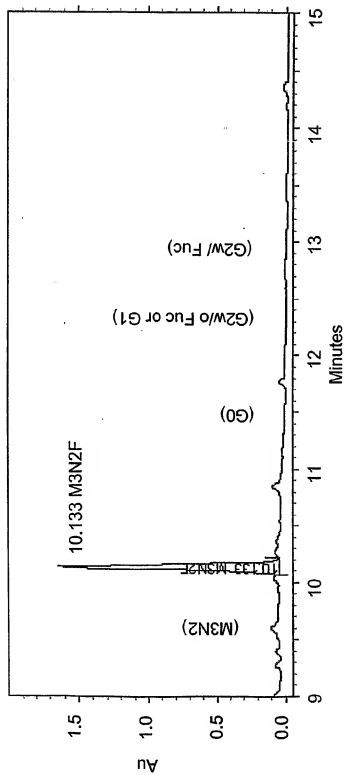


FIG. 99D

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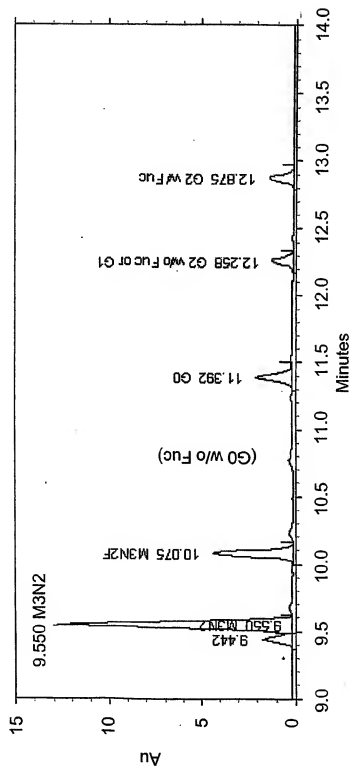


FIG. 100A

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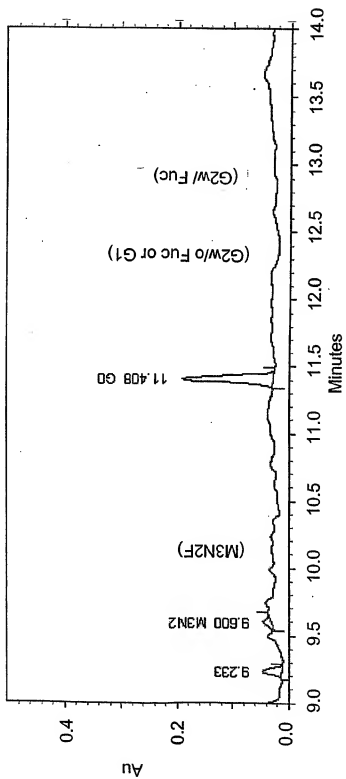


FIG. 100B

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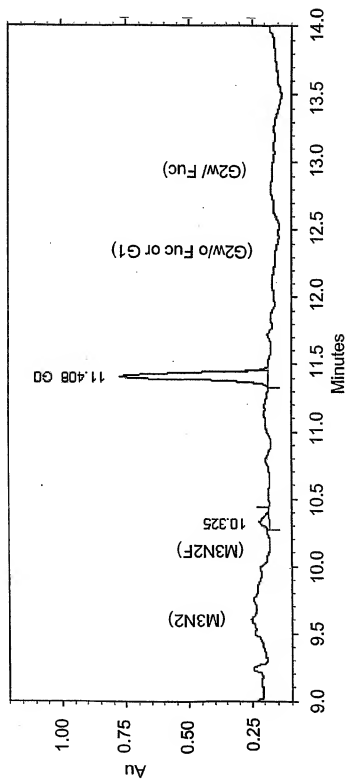


FIG. 100C

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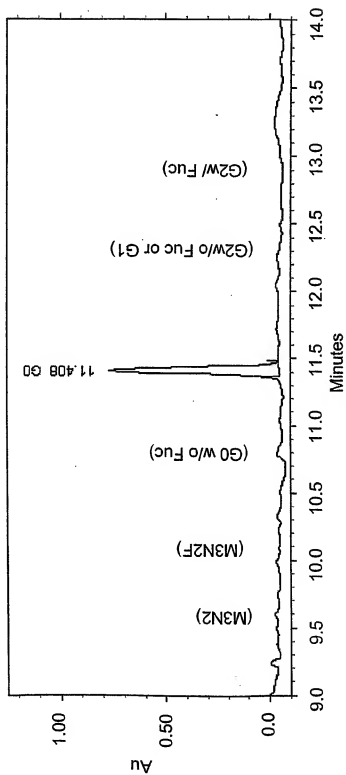


FIG. 100D



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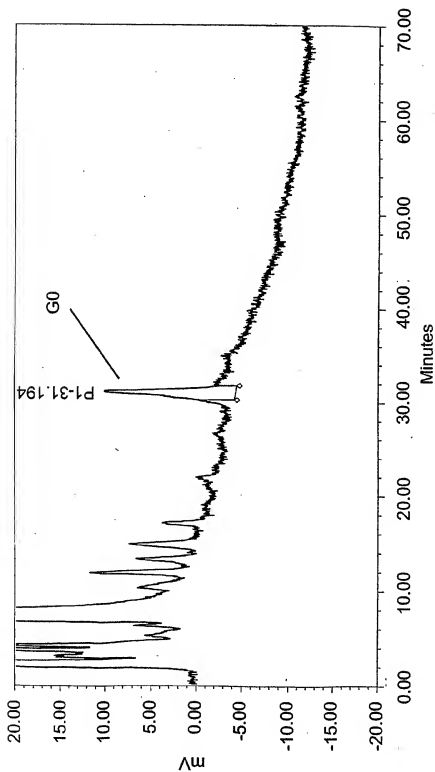


FIG. 101A

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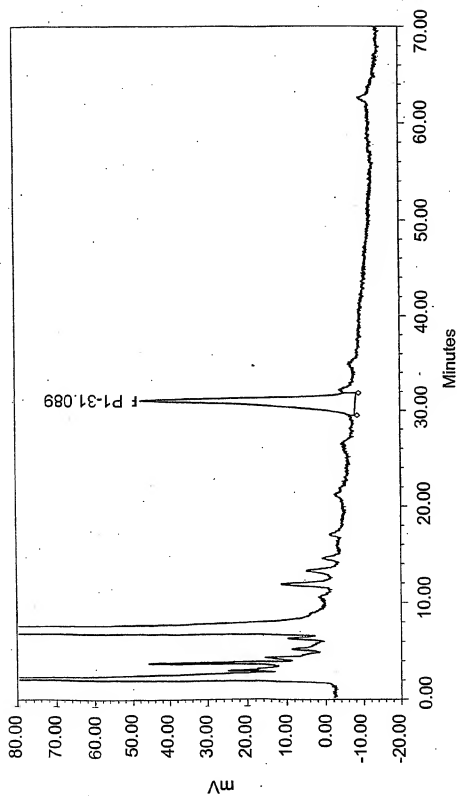


FIG. 101B

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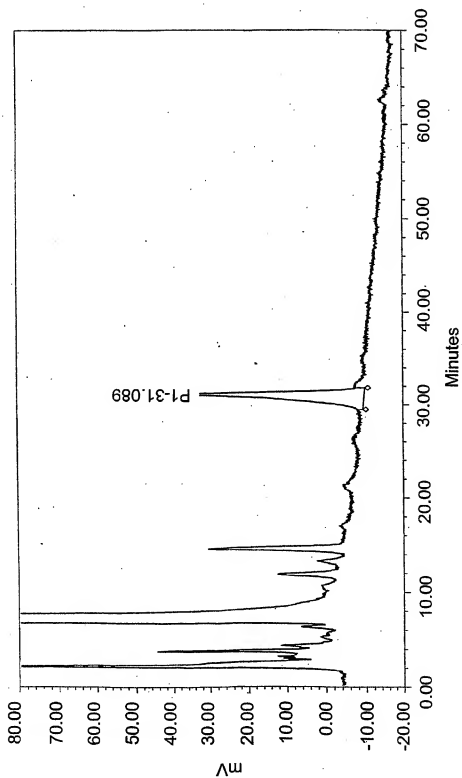


FIG. 101C

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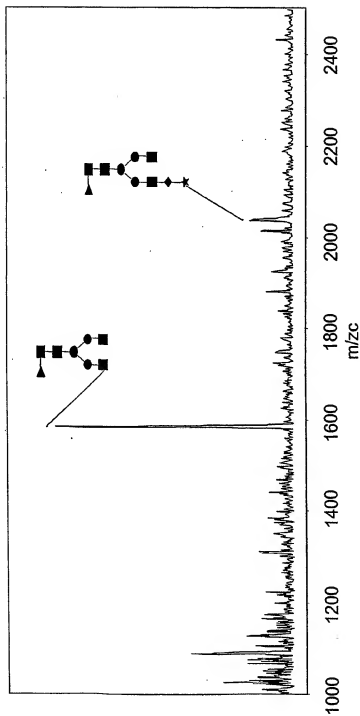


FIG. 102A

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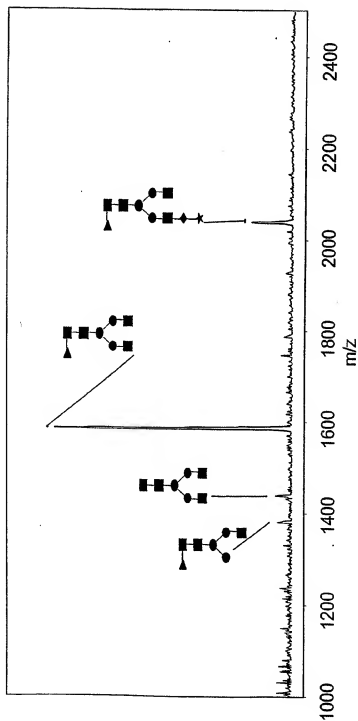


FIG. 102B



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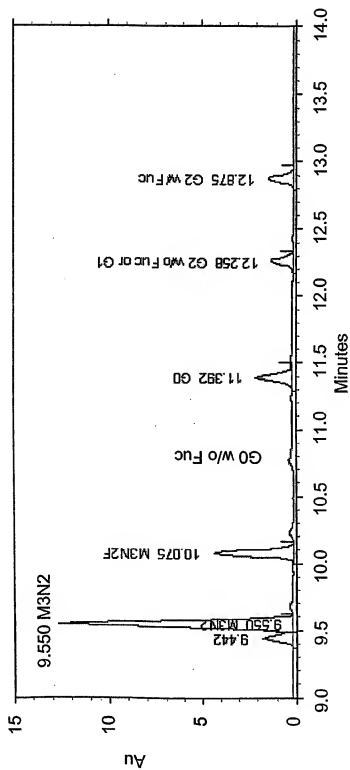


FIG. 103A

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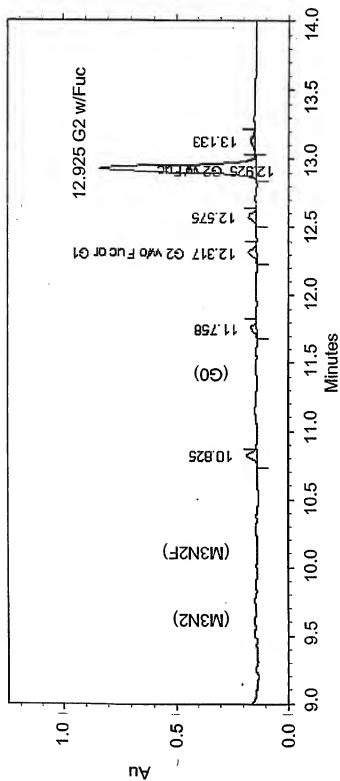


FIG. 103B



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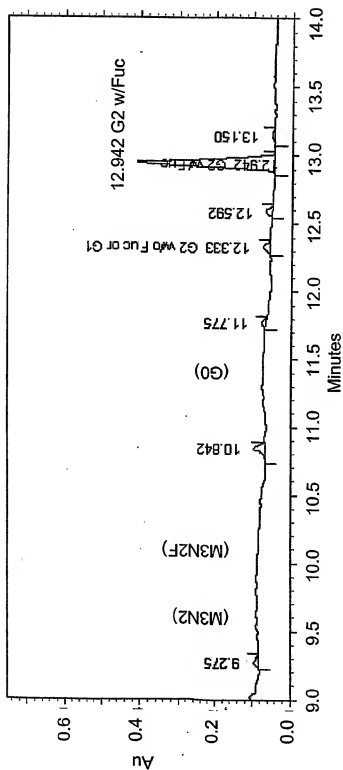


FIG. 103C

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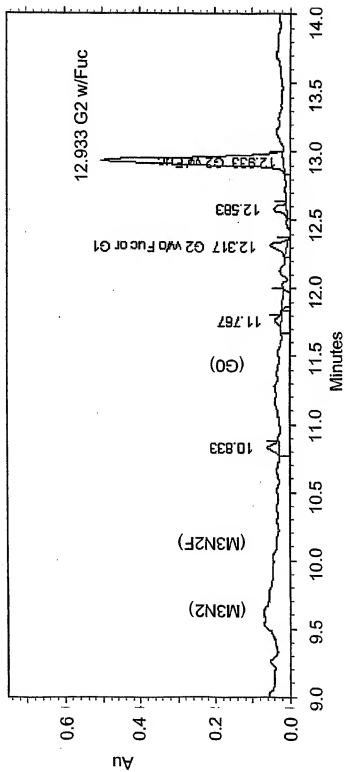


FIG. 103D

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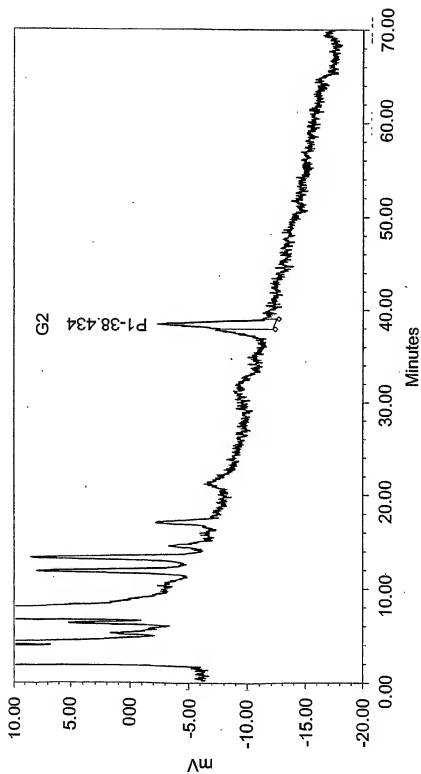


FIG. 104A

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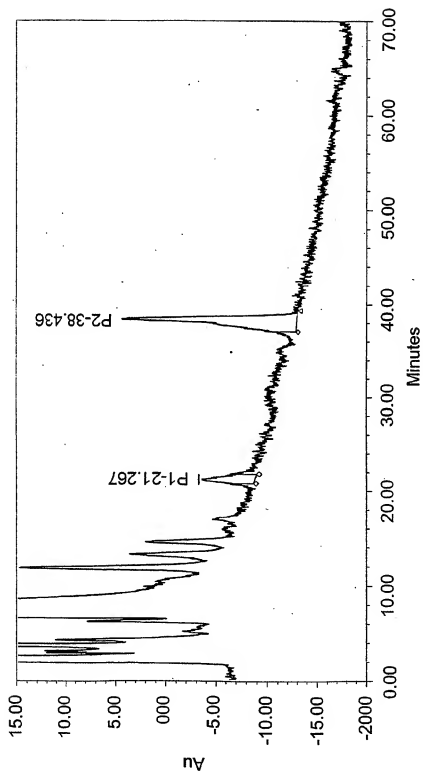


FIG. 104B

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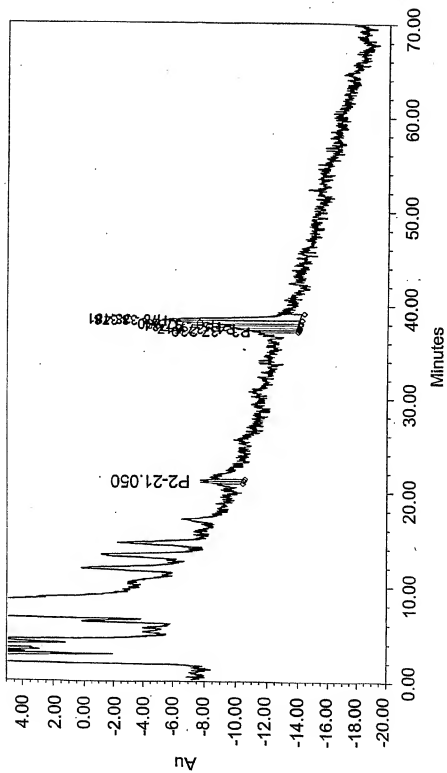


FIG. 104C

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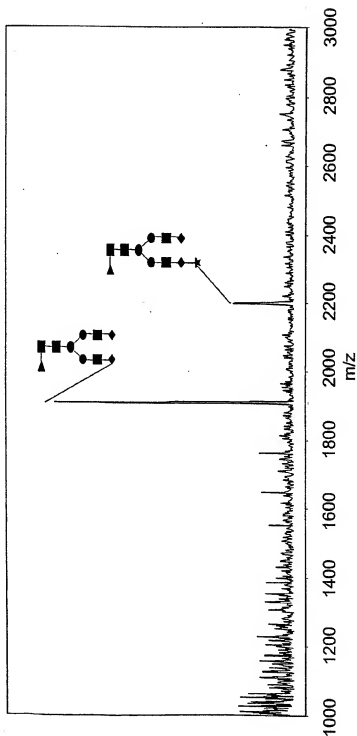


FIG. 105A

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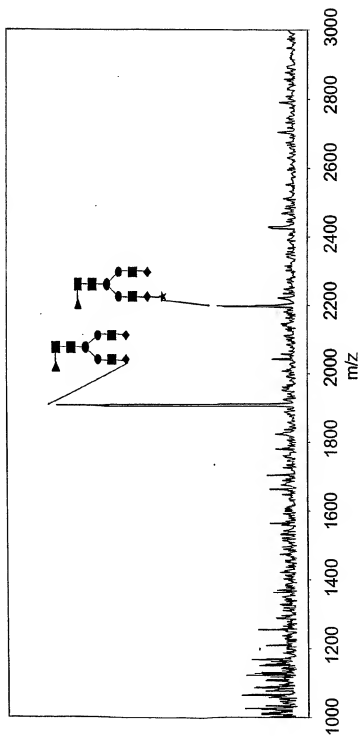


FIG. 105B

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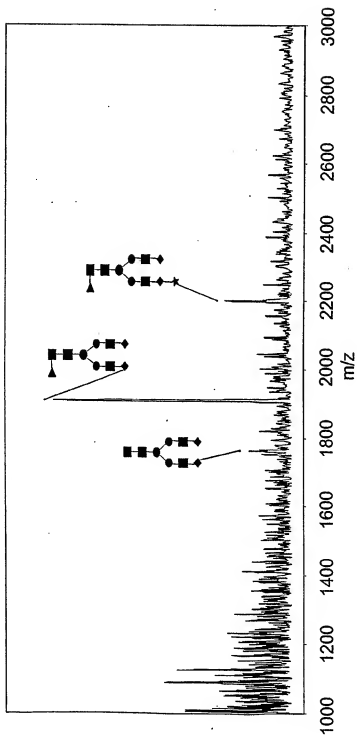


FIG. 105C



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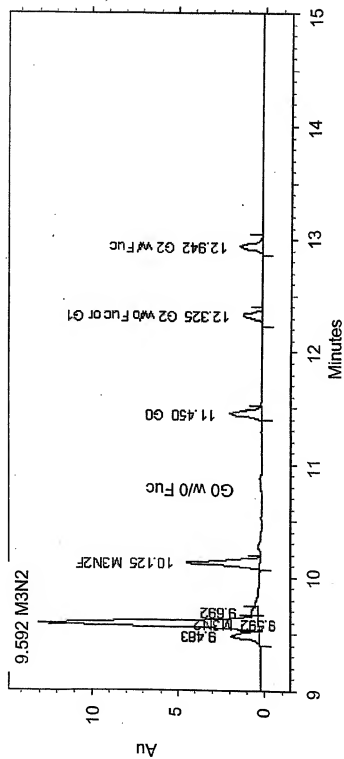


FIG. 106A

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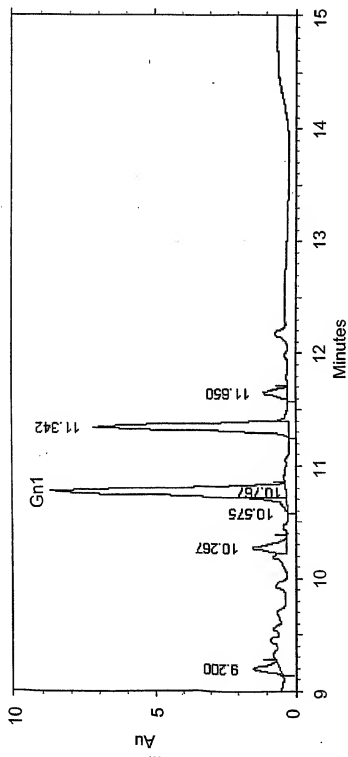


FIG. 106B

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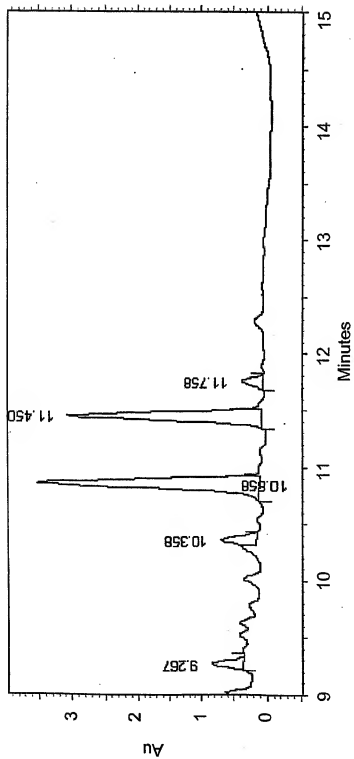


FIG. 106C

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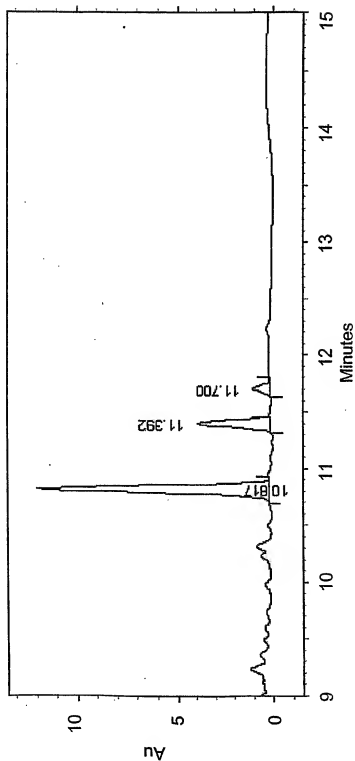


FIG. 106D

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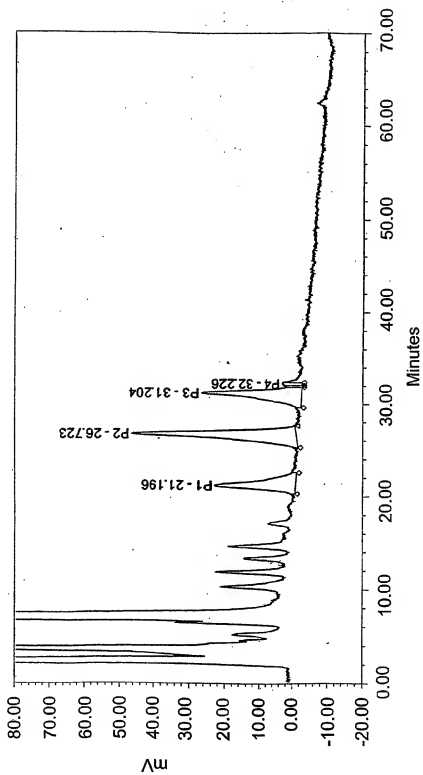


FIG. 107A

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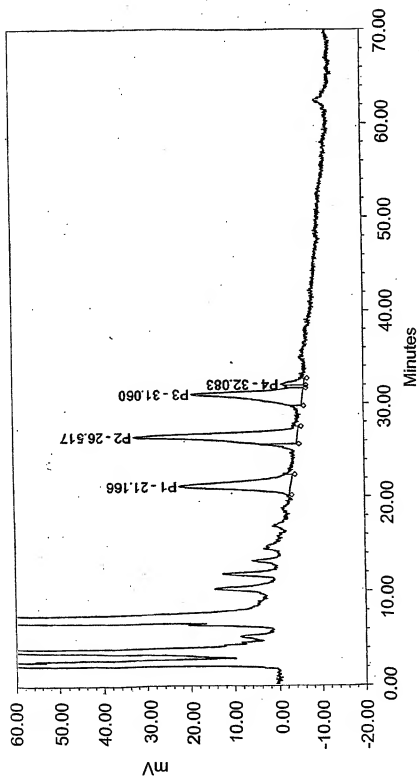


FIG. 107B

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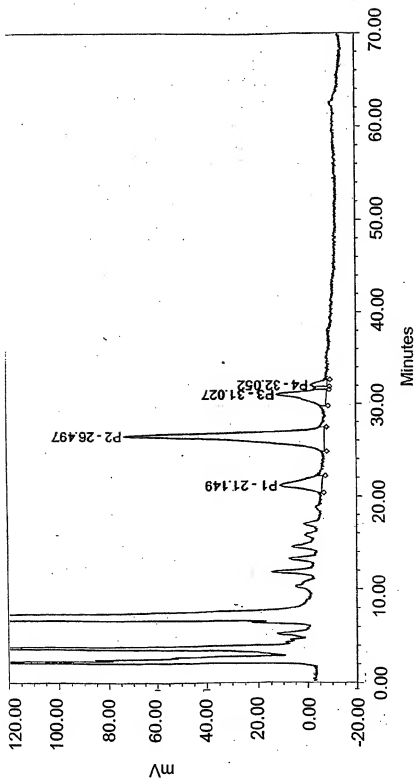


FIG. 107C

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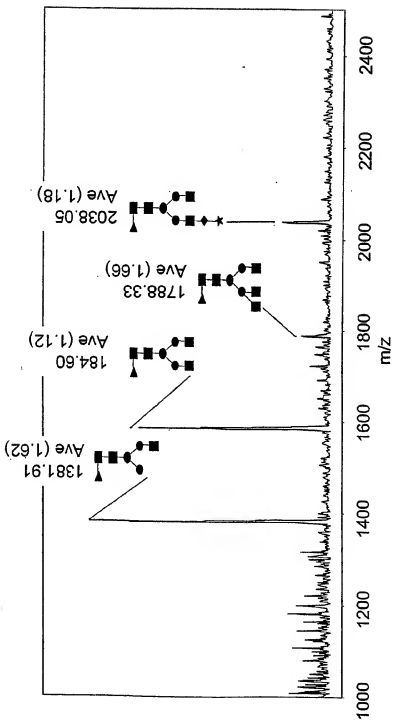


FIG. 108A



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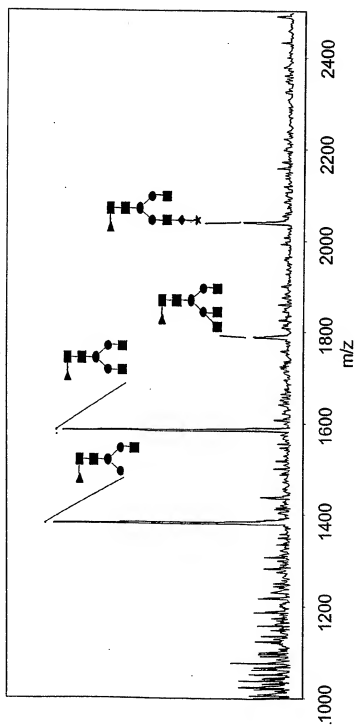


FIG. 108B

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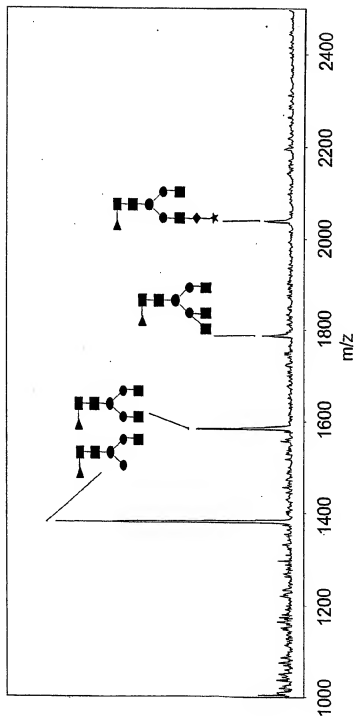


FIG. 108C

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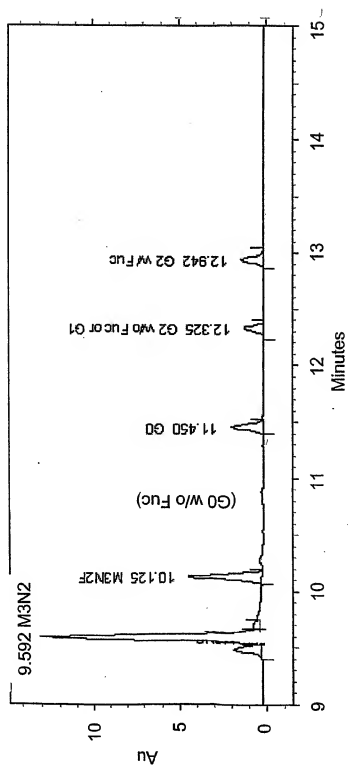


FIG. 109A

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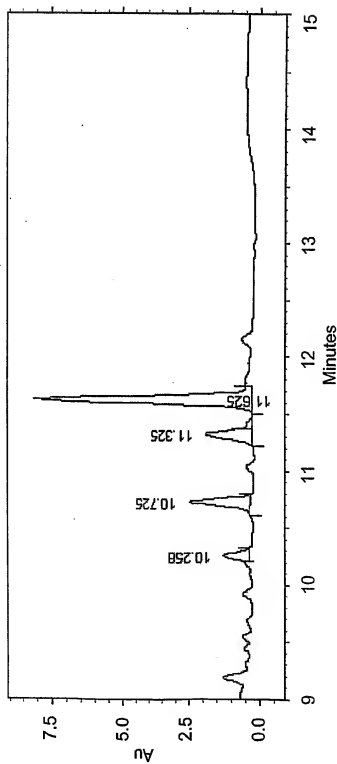


FIG. 109B

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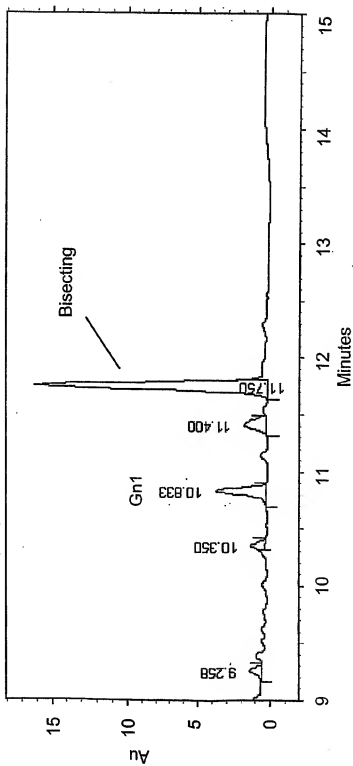


FIG. 109C

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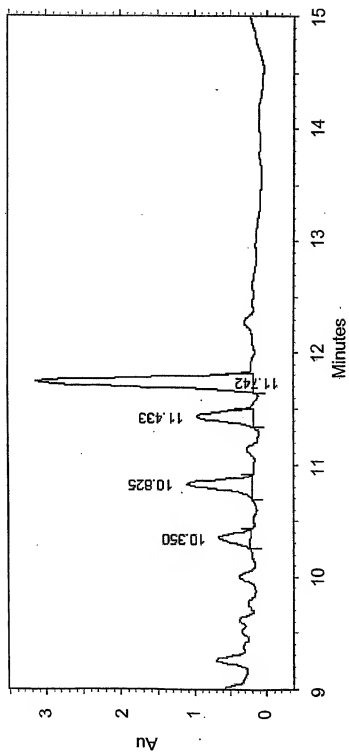


FIG. 109D

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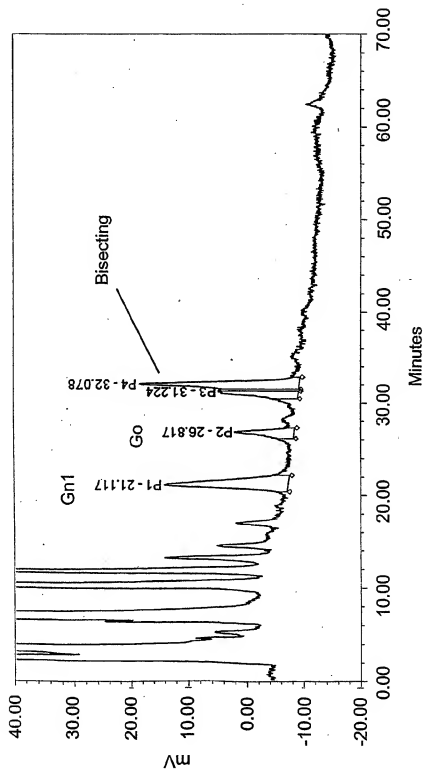


FIG. 110A

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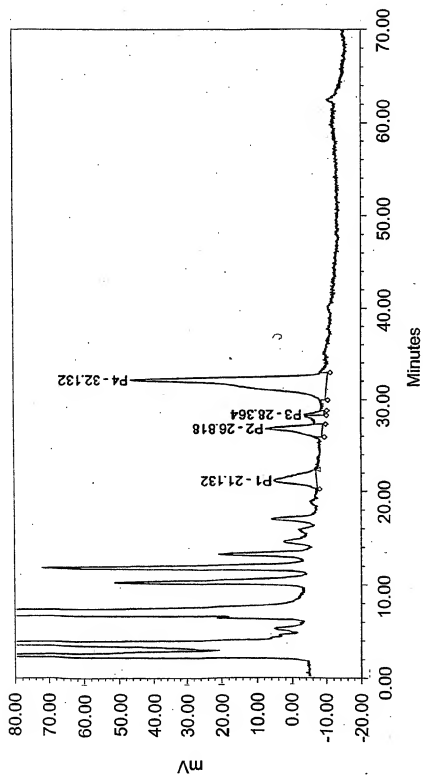


FIG. 110B



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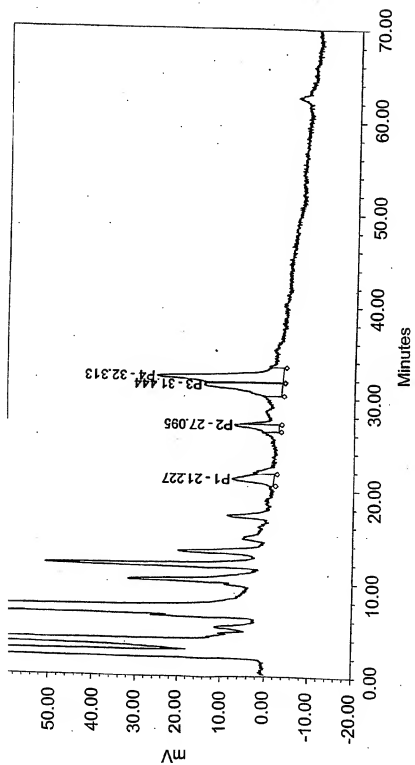


FIG. 110C

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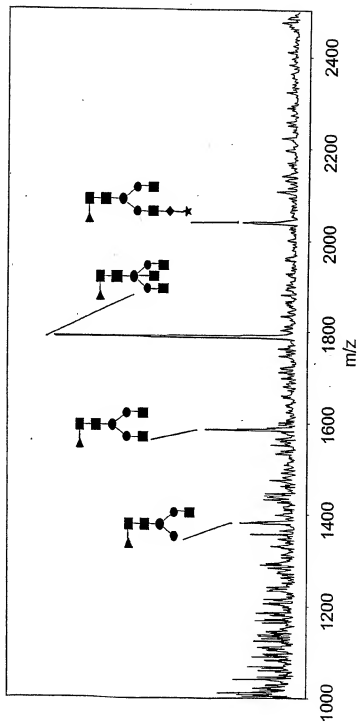


FIG. 111A

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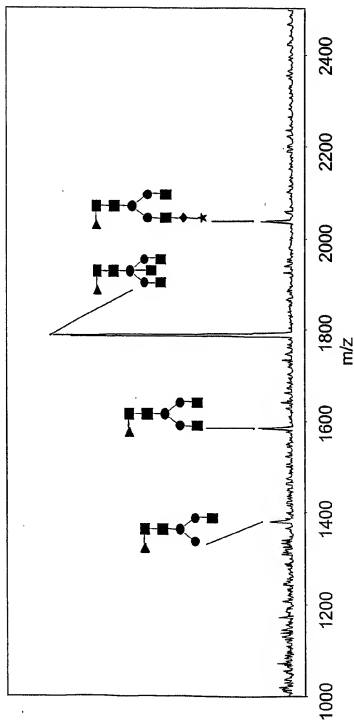


FIG. 111B

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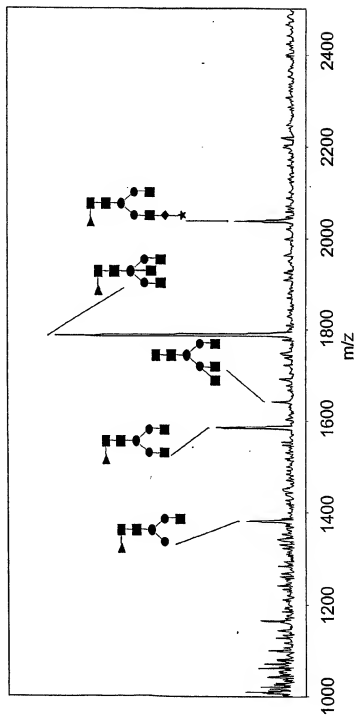


FIG. 111C

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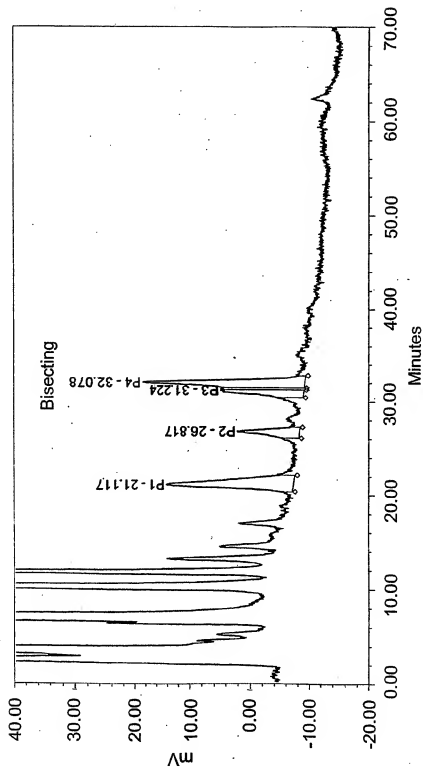


FIG. 112A

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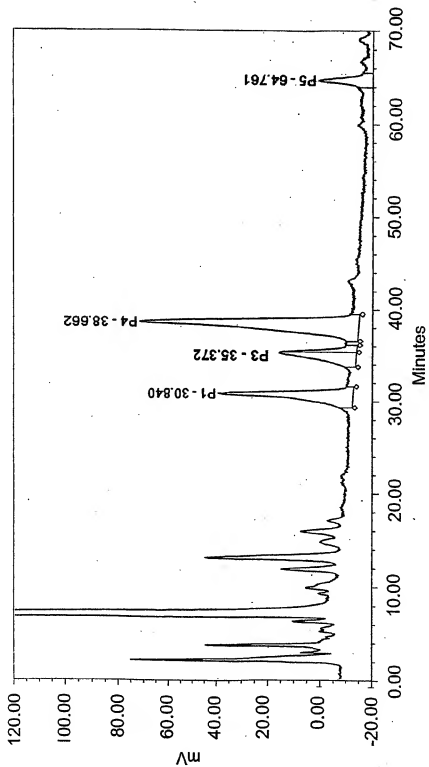


FIG. 112B

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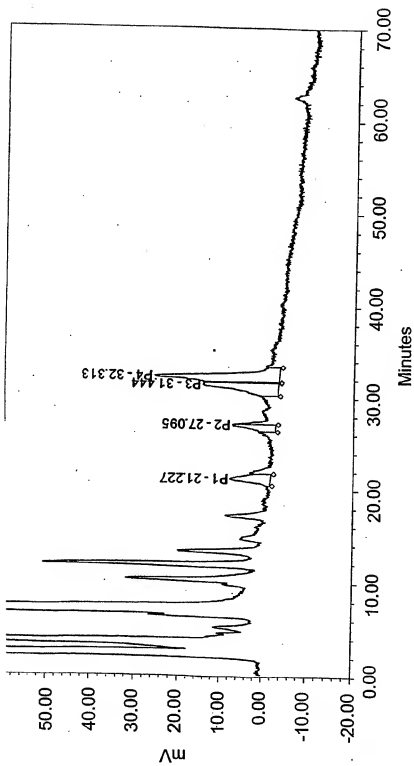


FIG. 112C

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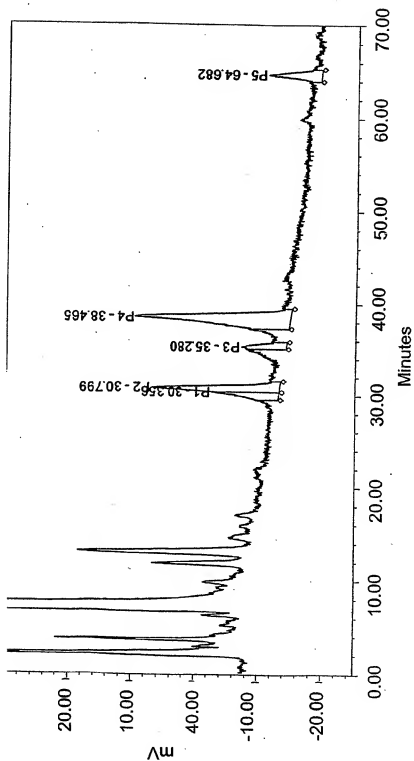


FIG. 112D



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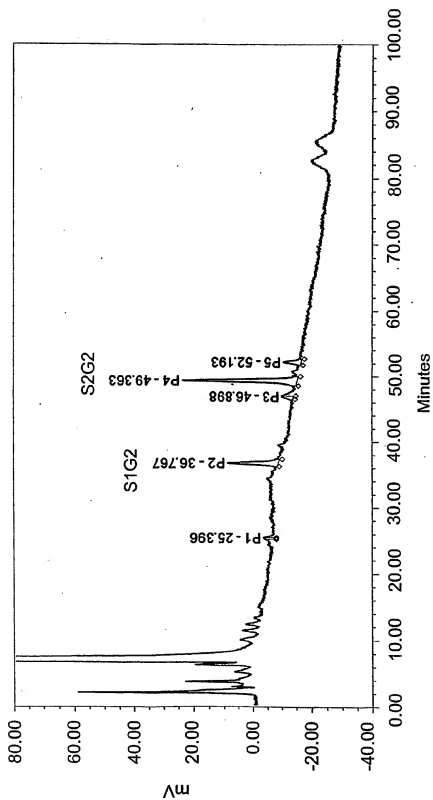


FIG. 113A

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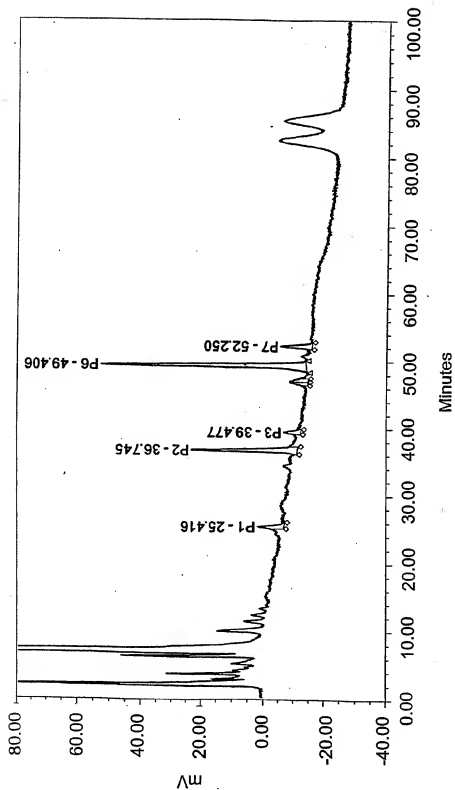


FIG. 113B

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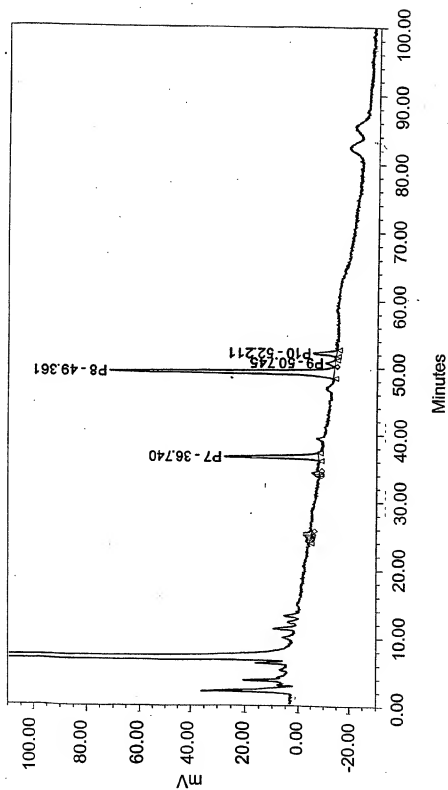


FIG. 113C

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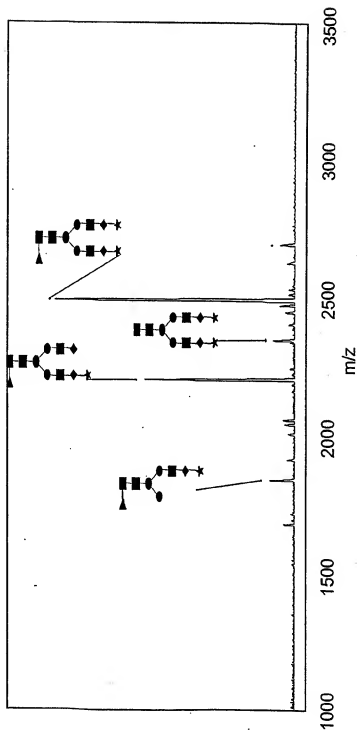


FIG. 114A

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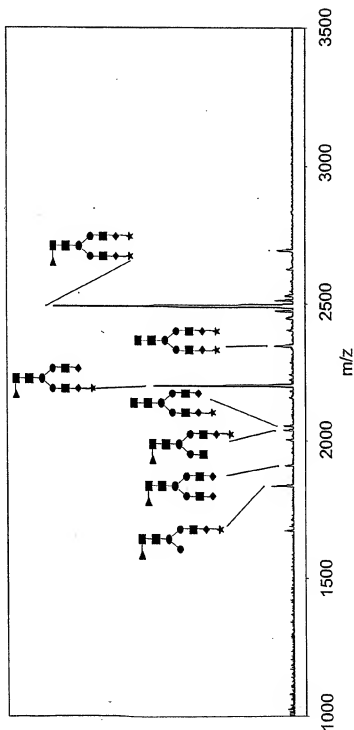


FIG. 114B

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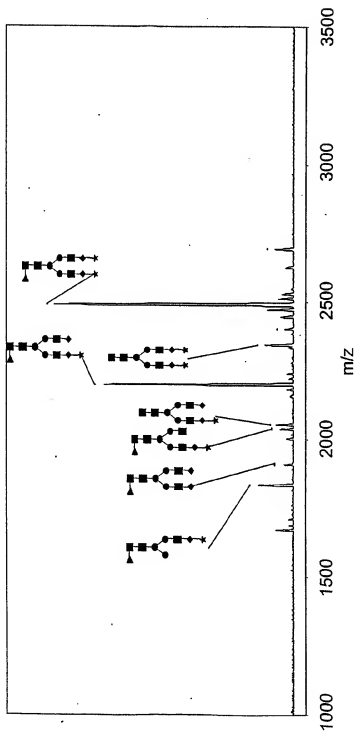


FIG. 114C

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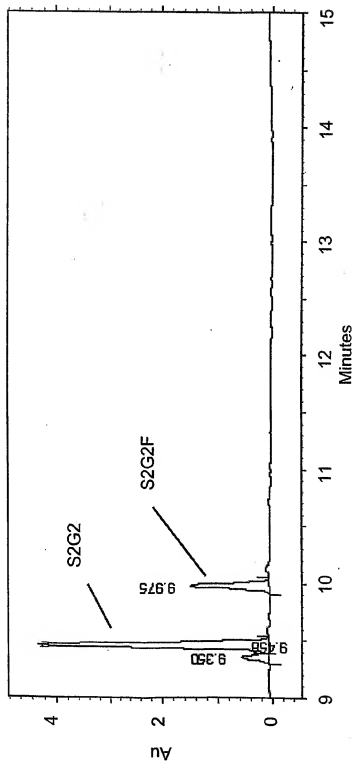


FIG. 115A

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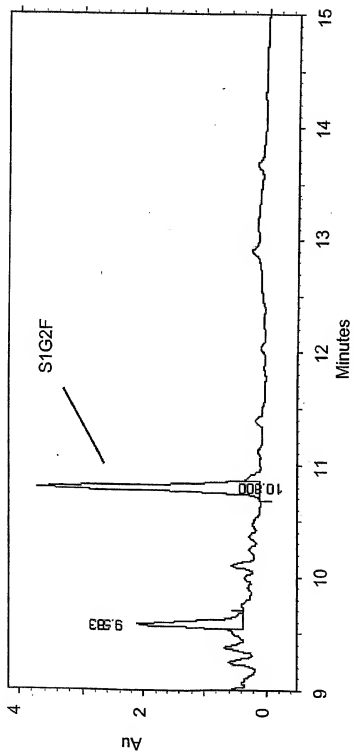


FIG. 115B



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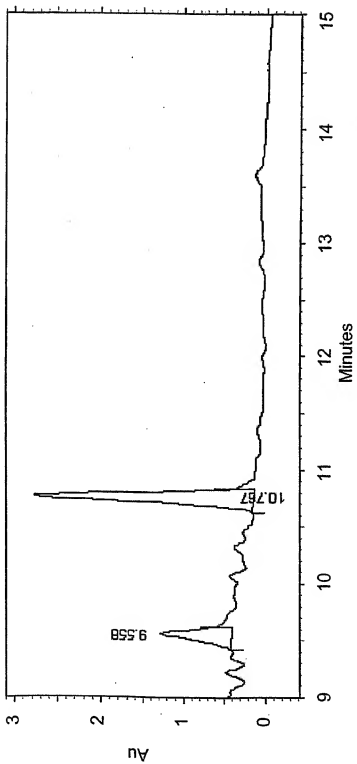


FIG. 115C

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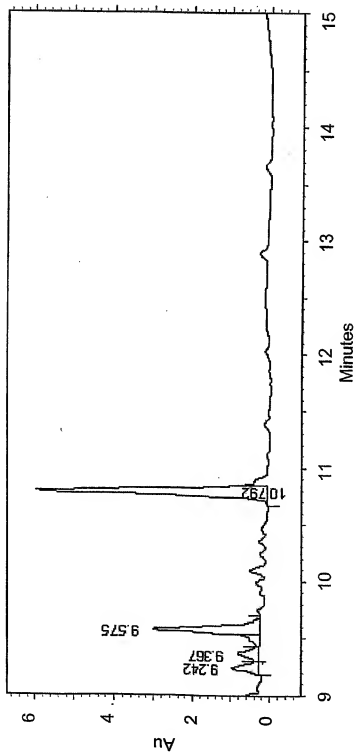


FIG. 115D

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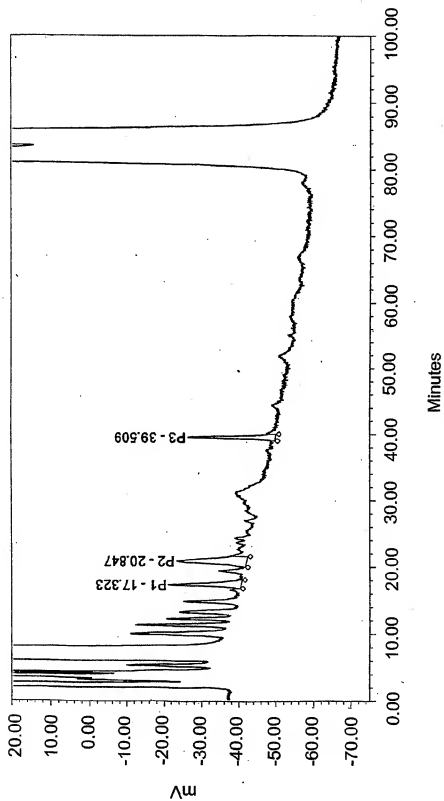


FIG. 116A

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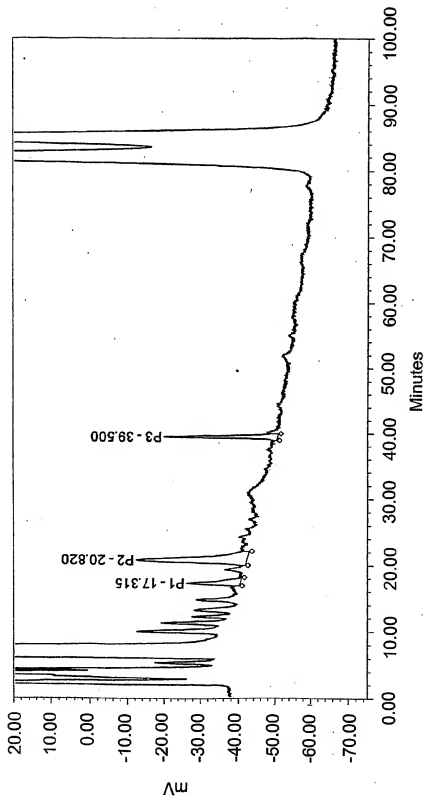


FIG. 116B

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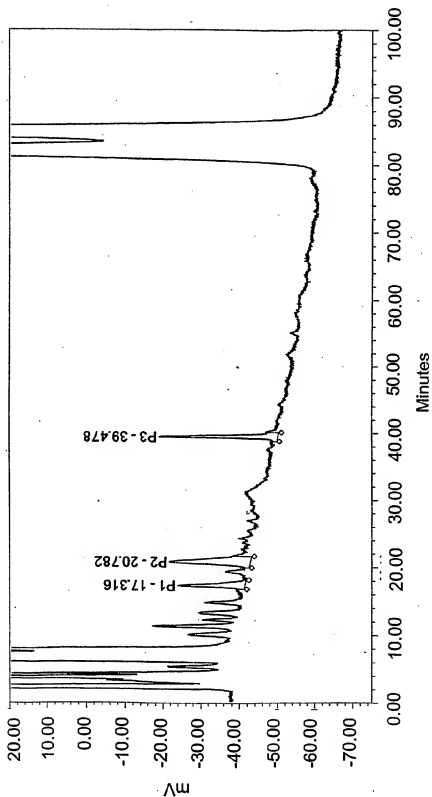


FIG. 116C

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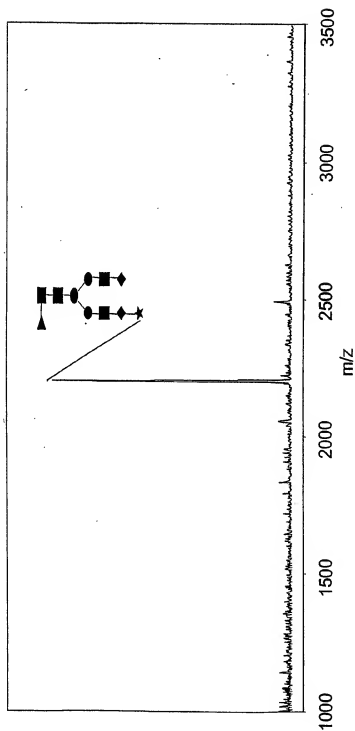


FIG. 117A

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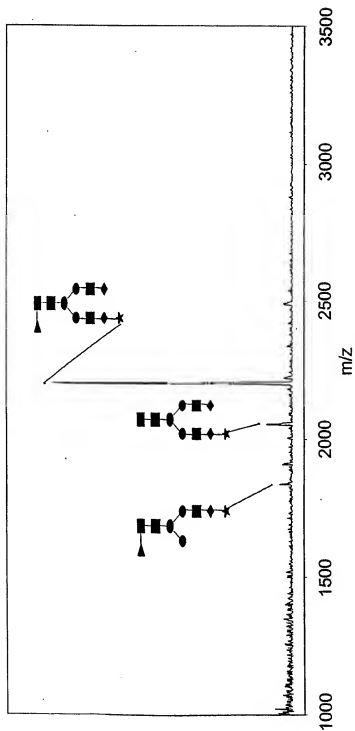


FIG. 117B

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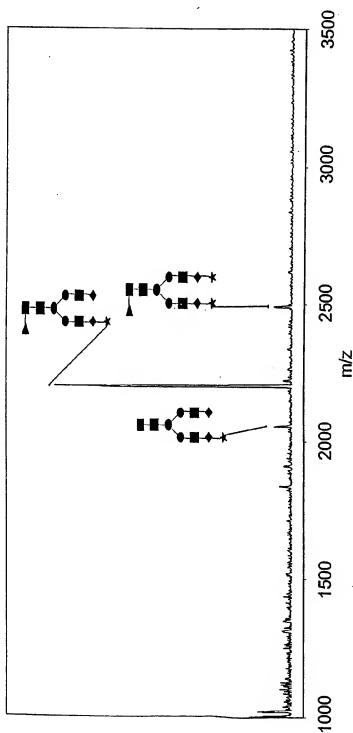


FIG. 117C



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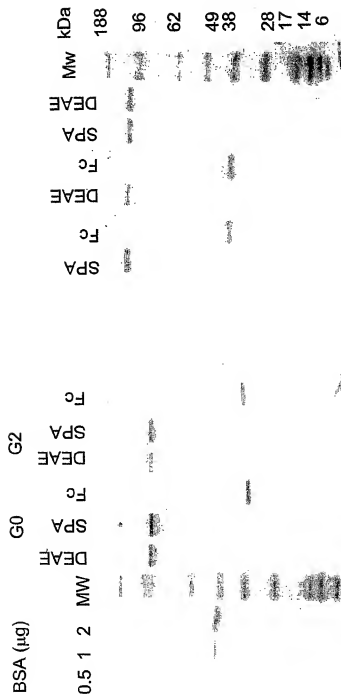


FIG. 118B

FIG. 118A

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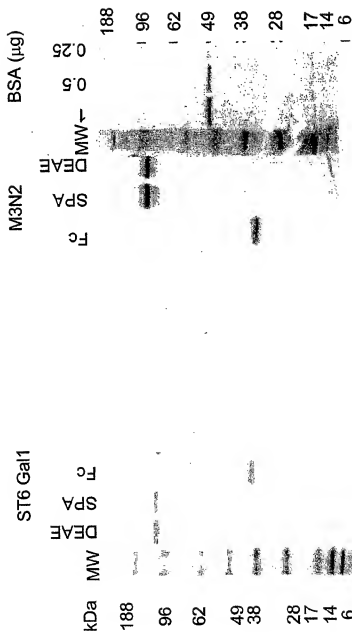


FIG. 118D

FIG. 118C

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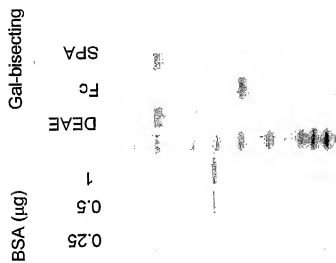


FIG. 118E

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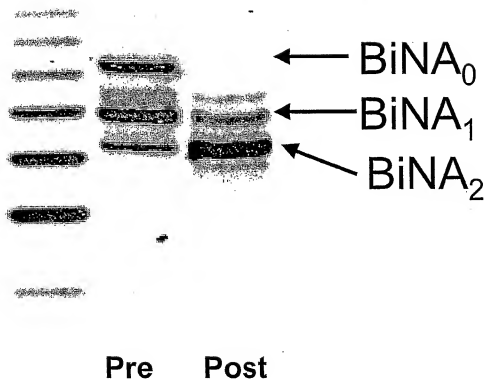


FIG. 119

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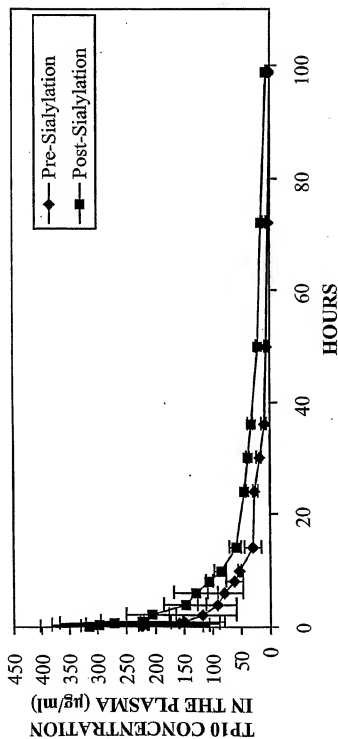


FIG. 120

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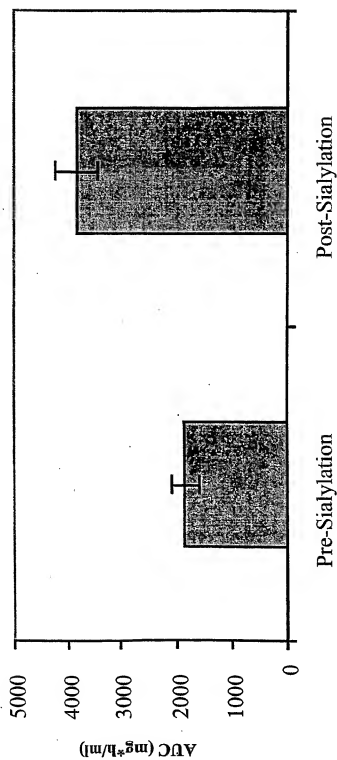


FIG. 121

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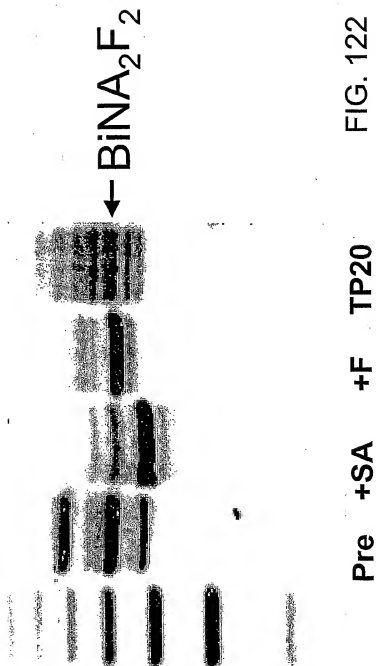


FIG. 122

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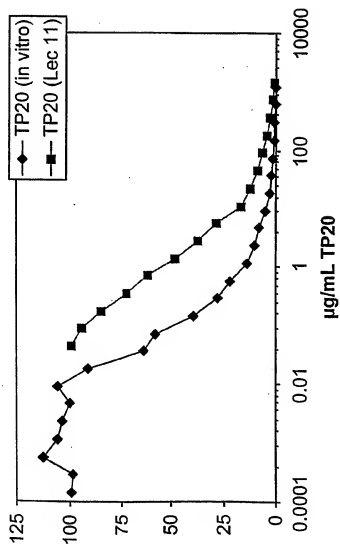


FIG. 123



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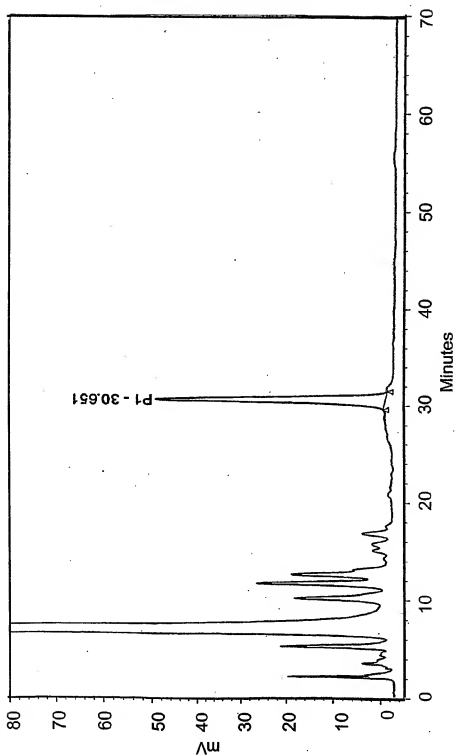


FIG. 124

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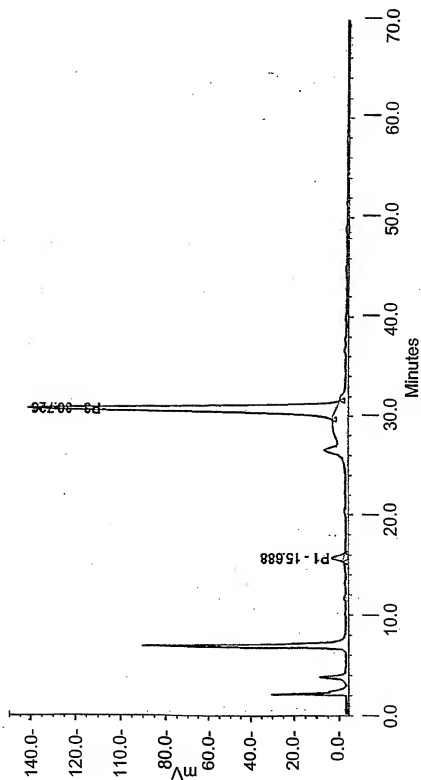


FIG. 125A

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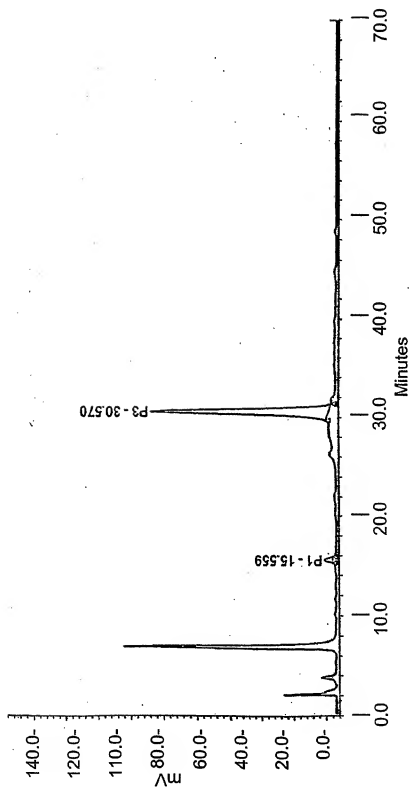


FIG. 125B

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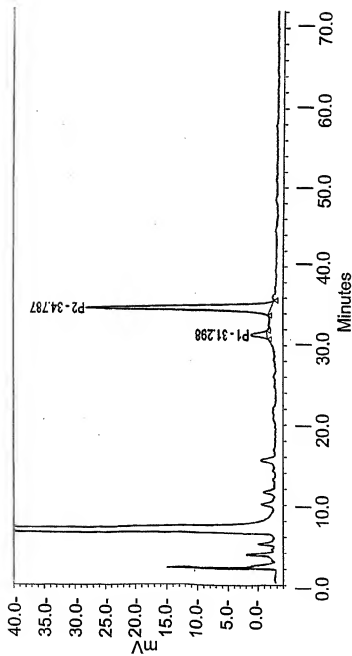


FIG. 126

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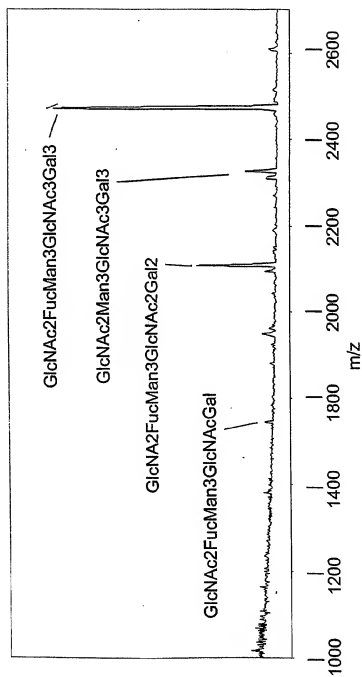


FIG. 127

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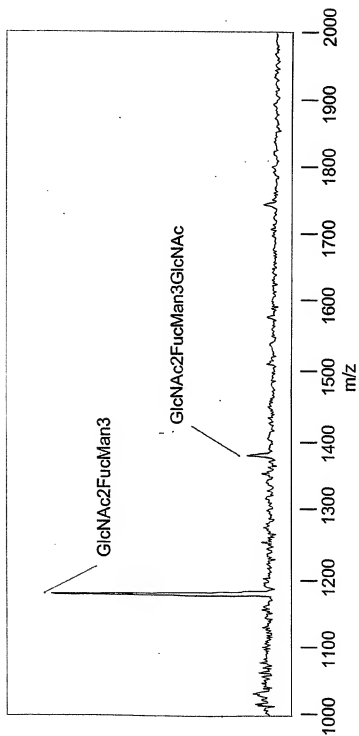


FIG. 128

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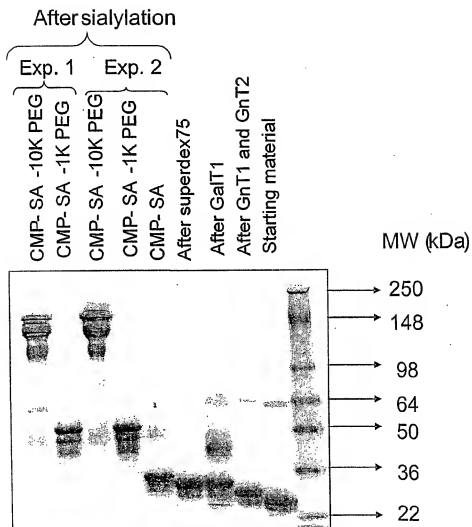


FIG. 129

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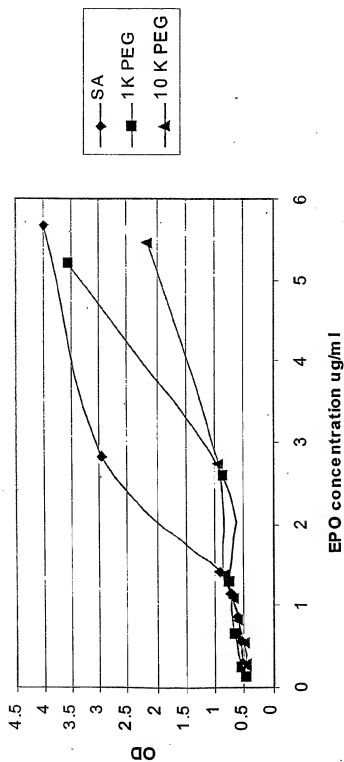
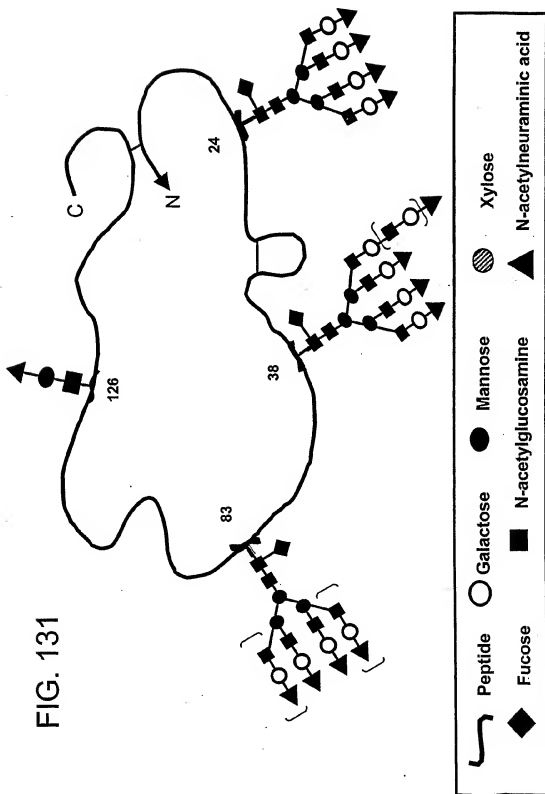


FIG. 130

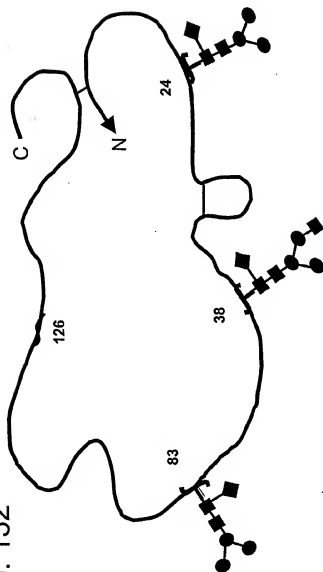


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FIG. 132



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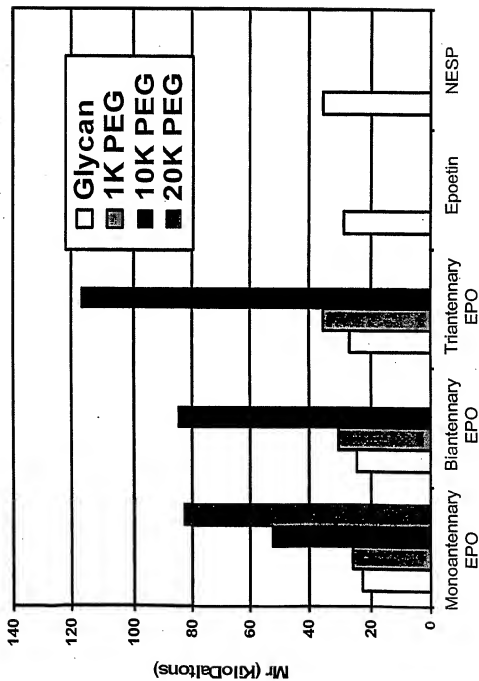
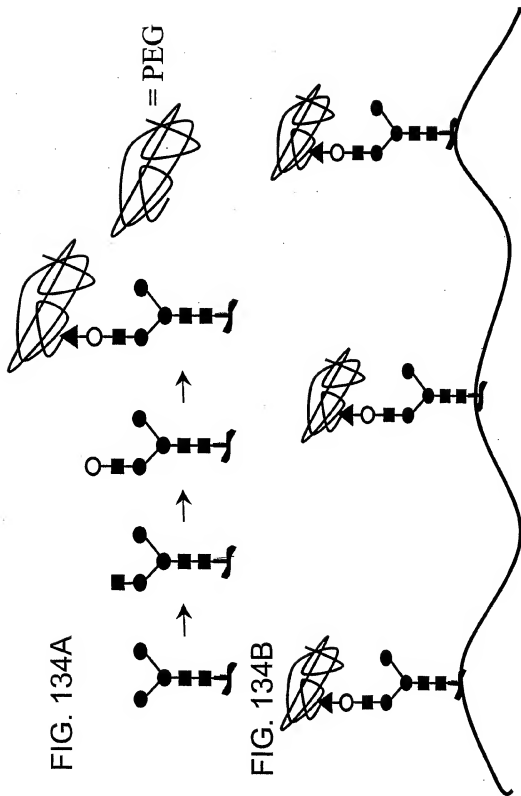


FIG. 133

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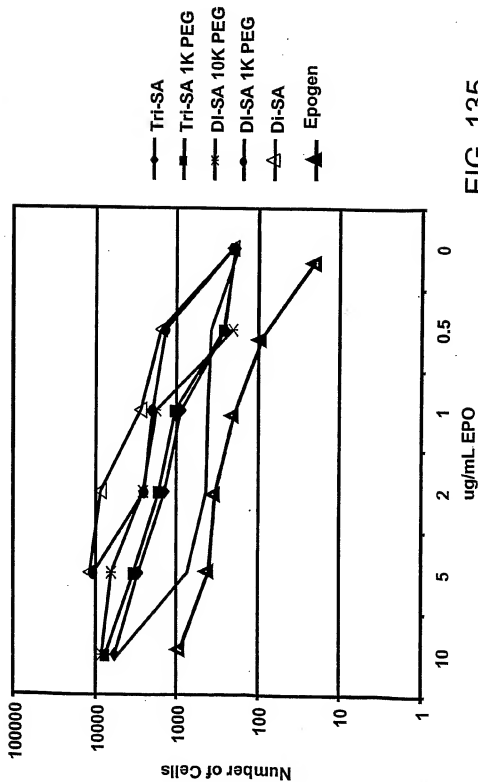


FIG. 135

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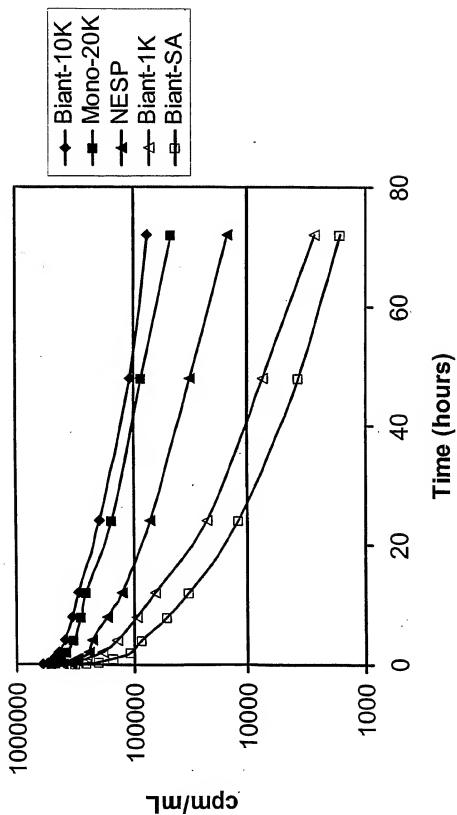


FIG. 136

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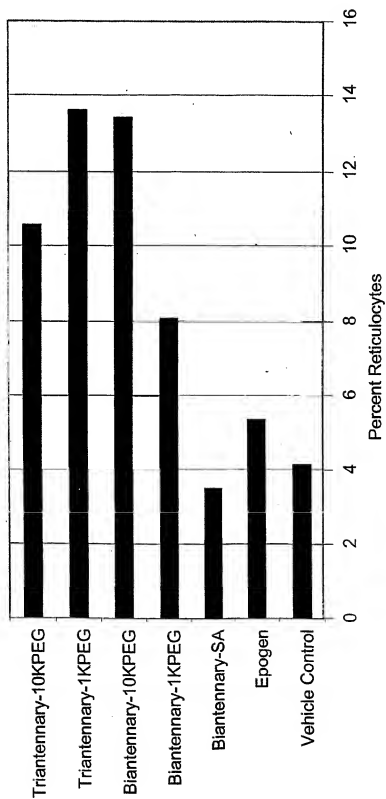


FIG. 137

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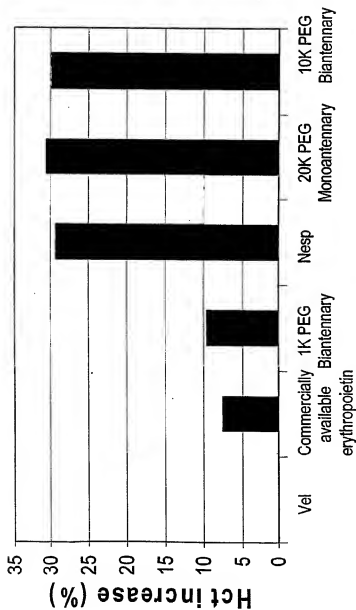


FIG. 138



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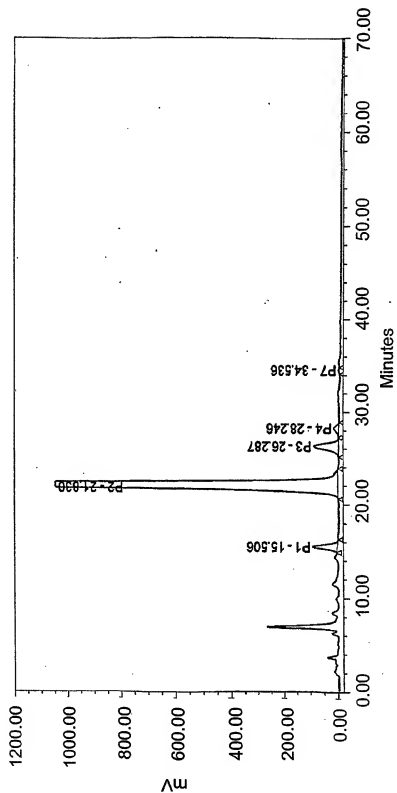


FIG. 139A

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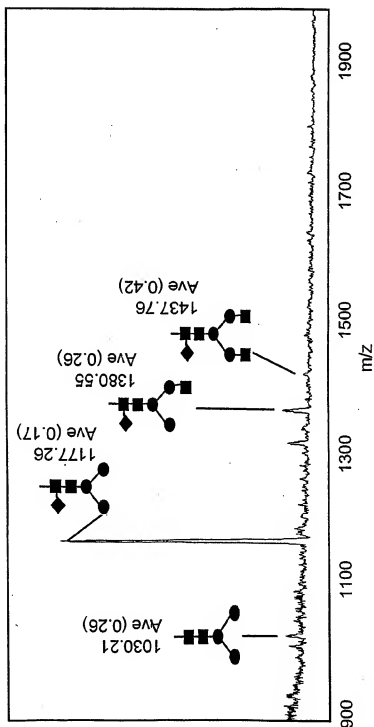


FIG. 139B

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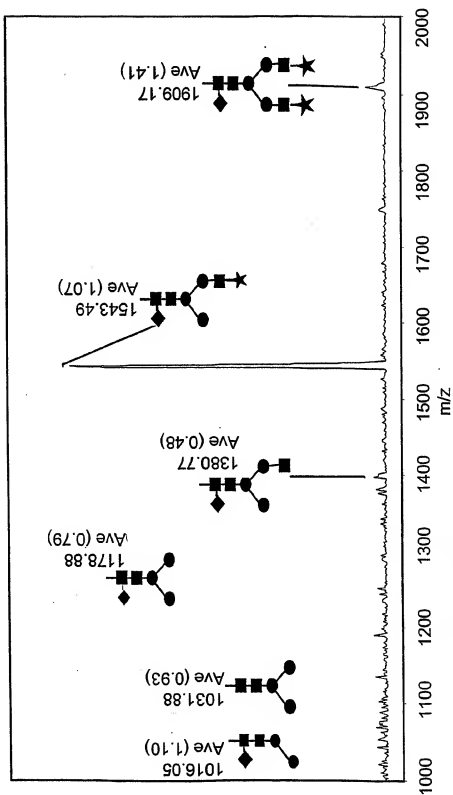


FIG. 140

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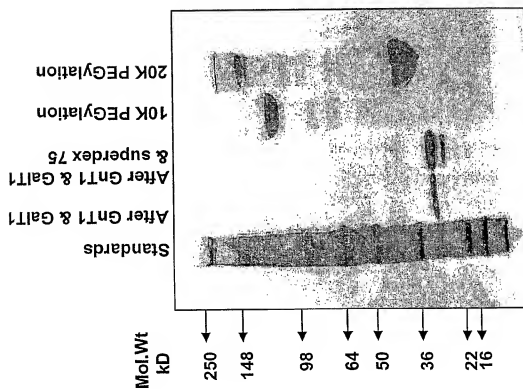


FIG. 141

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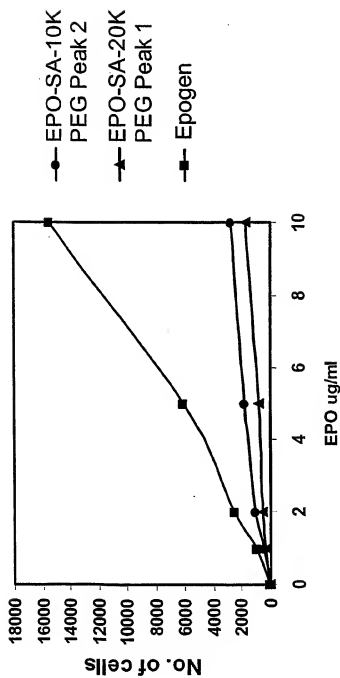


FIG. 142

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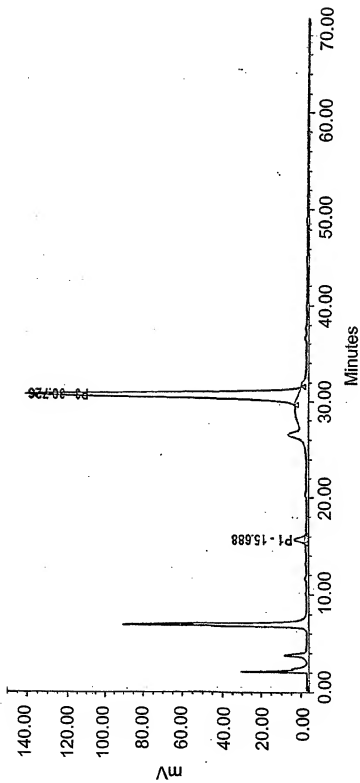


FIG. 143A

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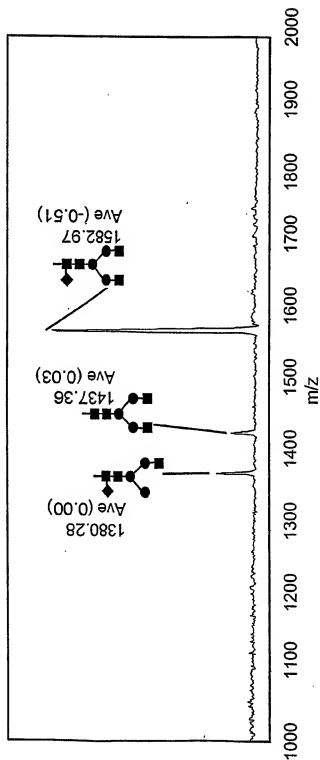


FIG. 143B

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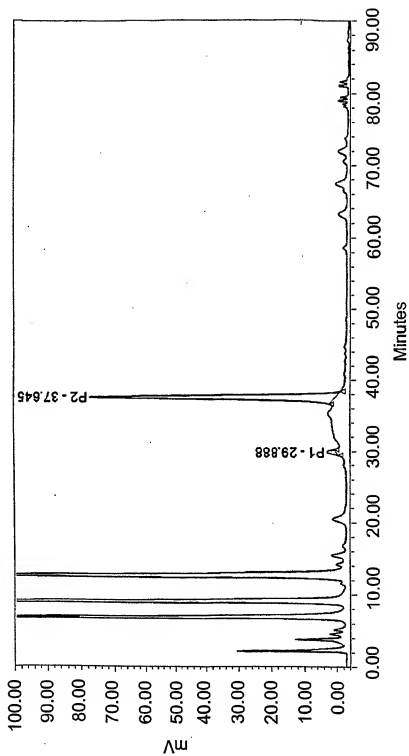


FIG. 144A



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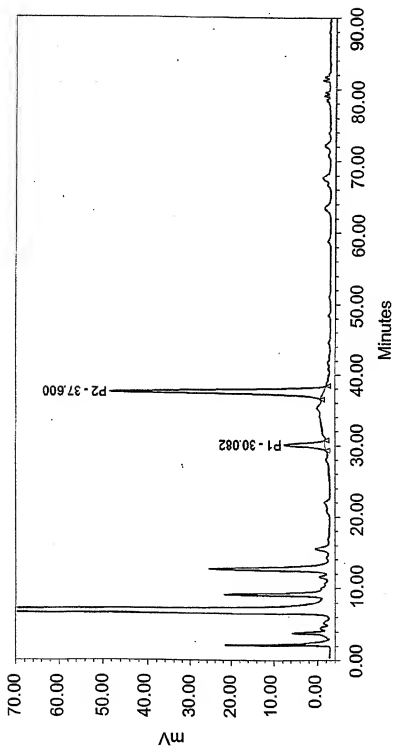


FIG. 144B

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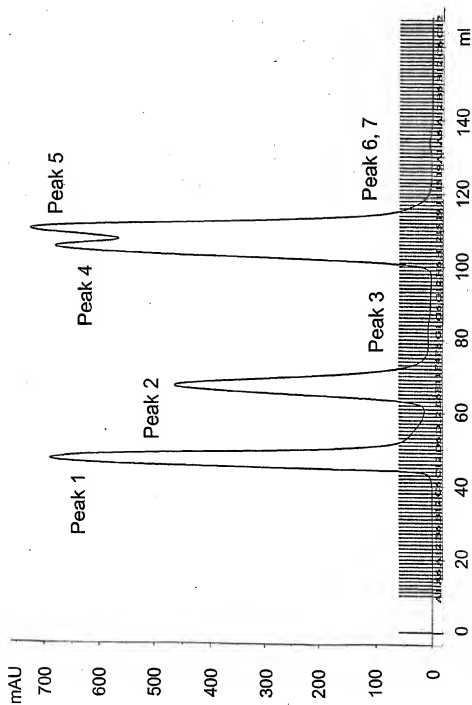


FIG. 145

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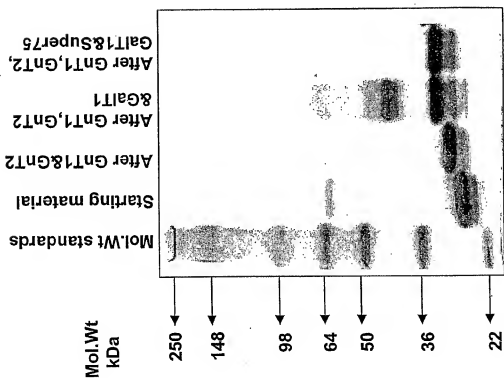


FIG. 146

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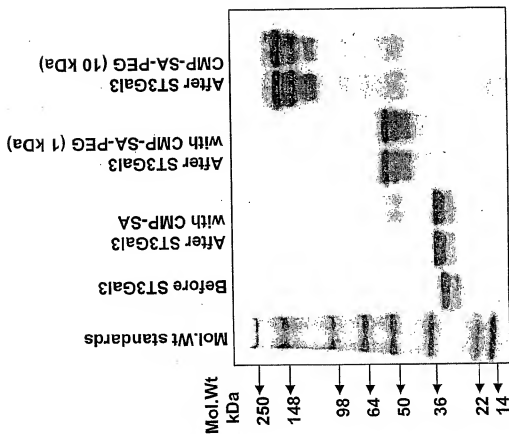


FIG. 147

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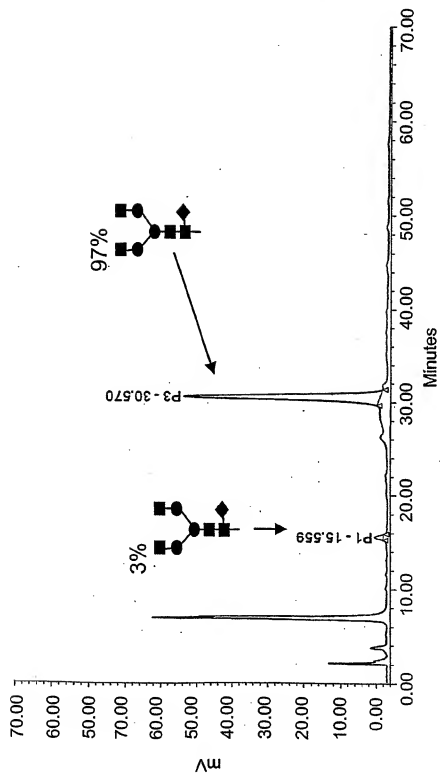


FIG. 148

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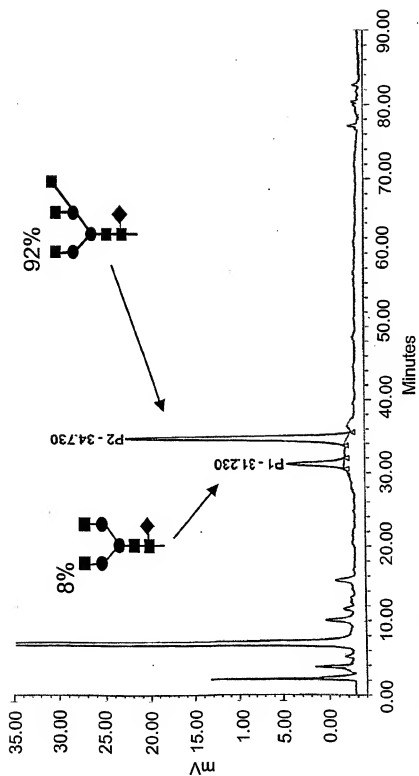


FIG. 149

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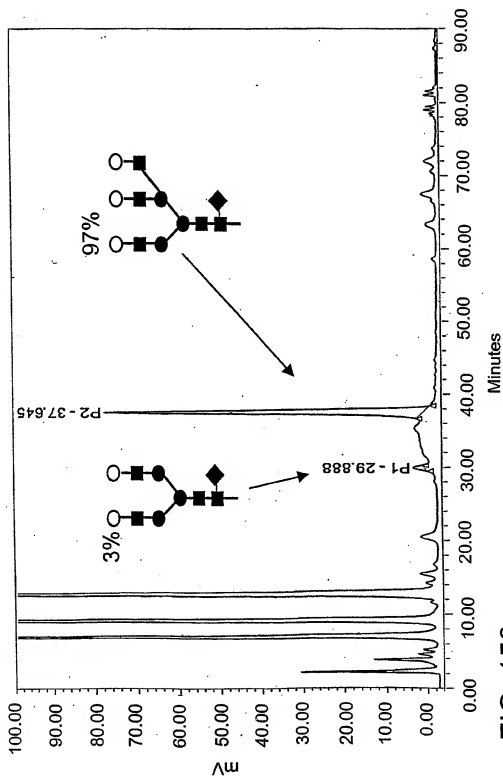


FIG. 150

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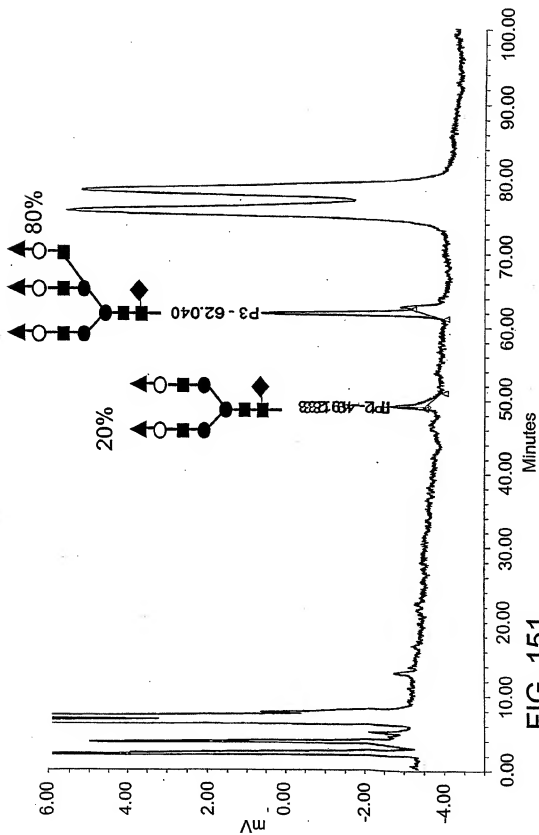


FIG. 151



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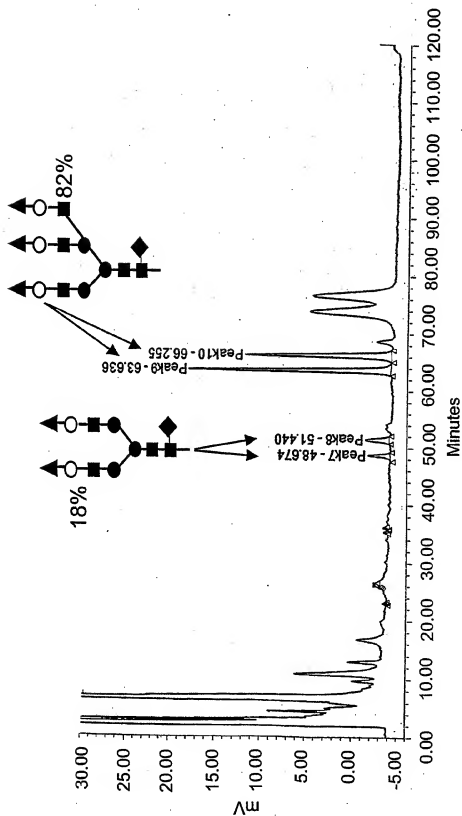


FIG. 152

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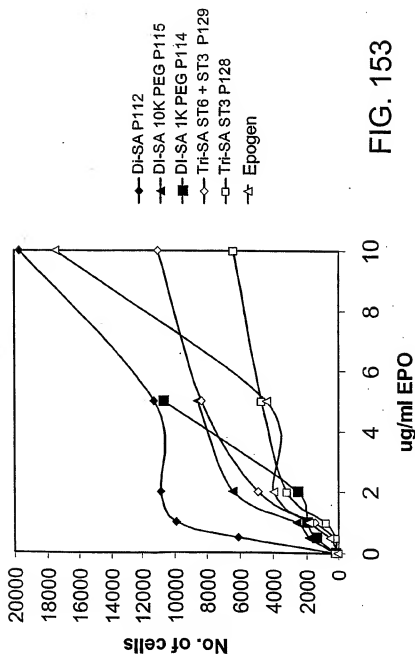


FIG. 153

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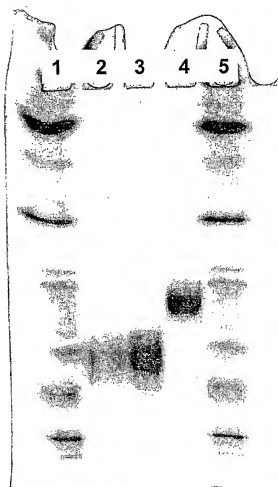


FIG. 154

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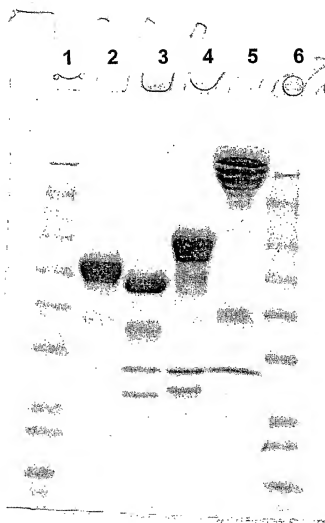


FIG. 155

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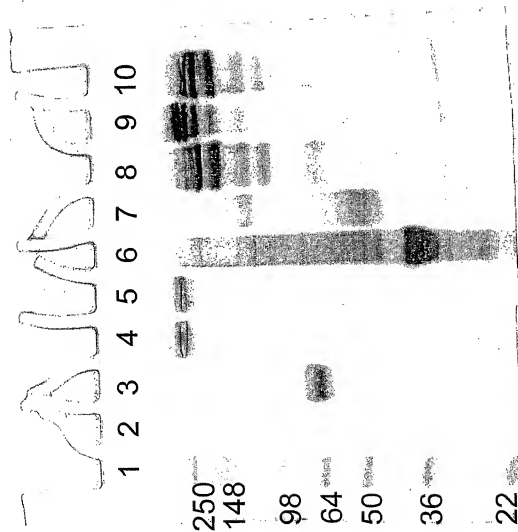


FIG. 156

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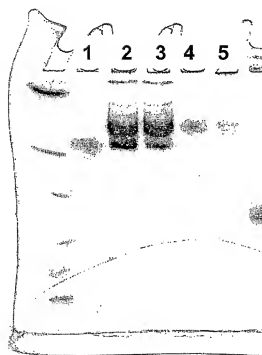


FIG. 157

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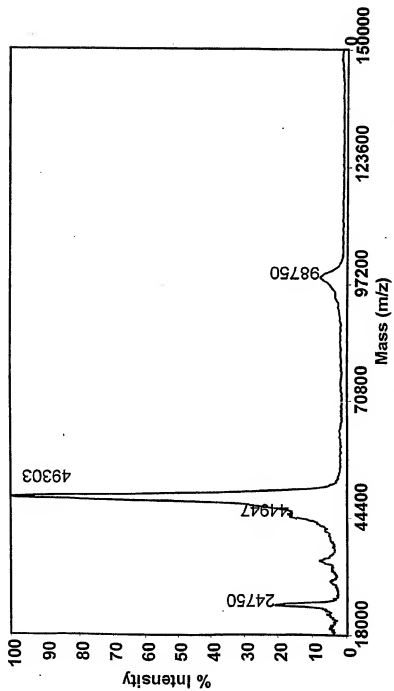


FIG. 158

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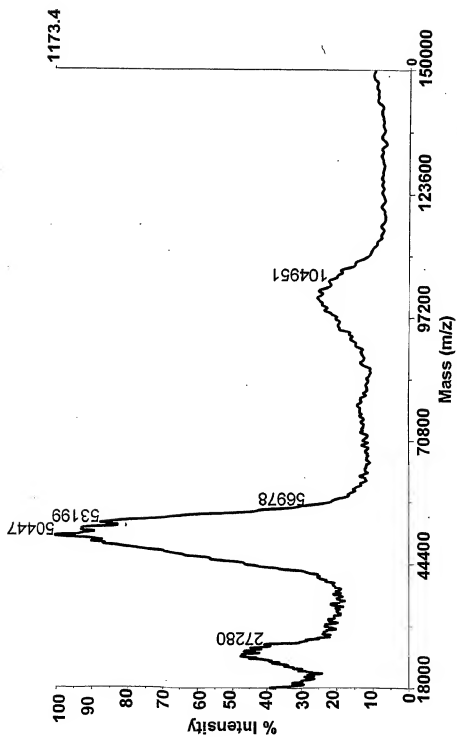


FIG. 159



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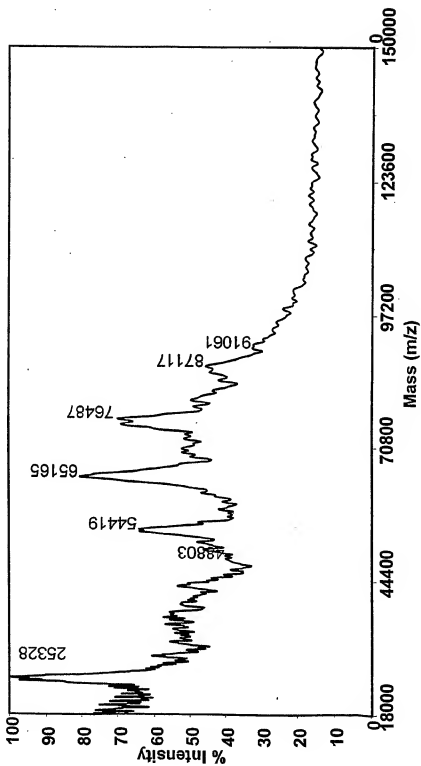


FIG. 160

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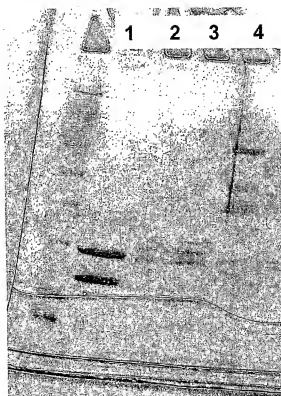


FIG. 161

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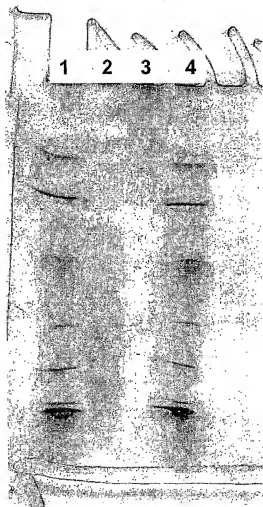


FIG. 162

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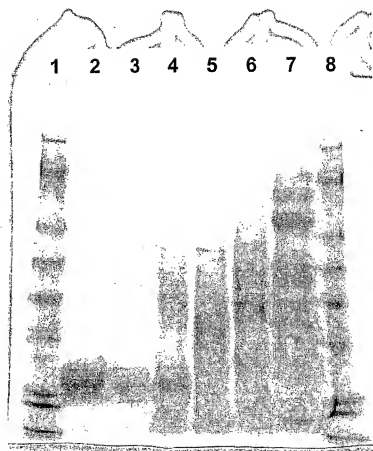


FIG. 163

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FIG. 164

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FIG. 165

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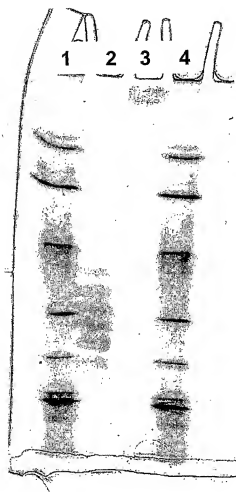


FIG. 166

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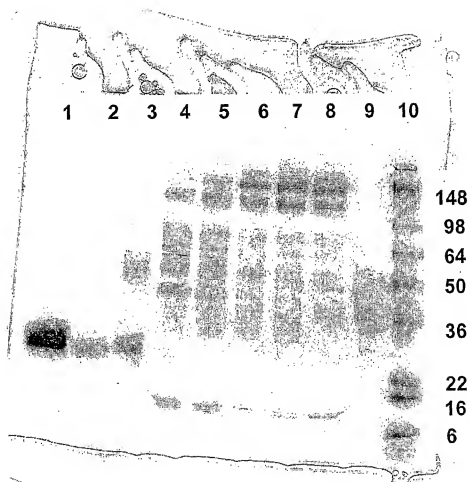


FIG. 167



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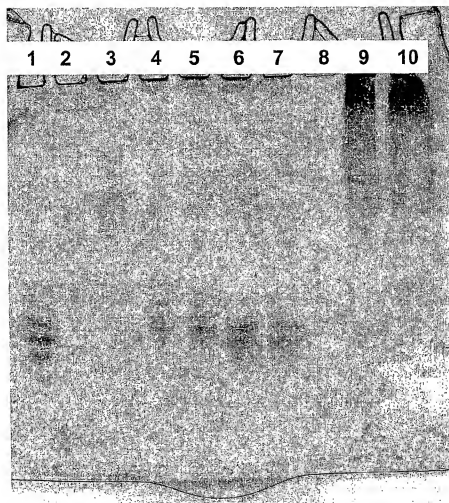
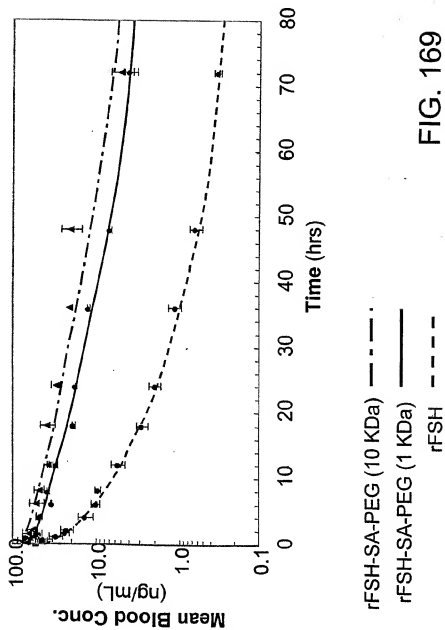


FIG. 168

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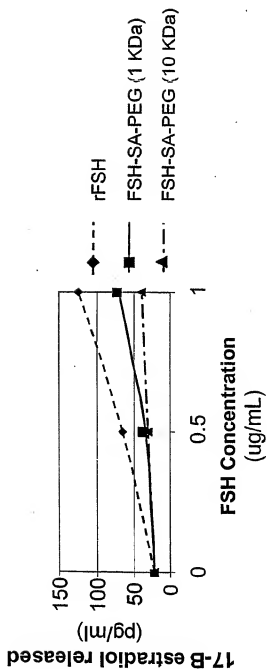


FIG. 170

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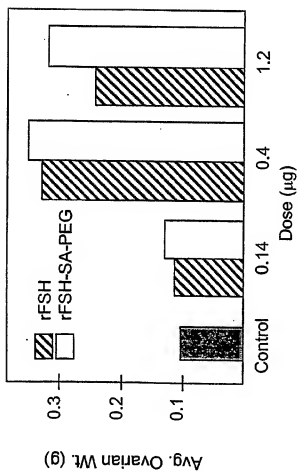


FIG. 171

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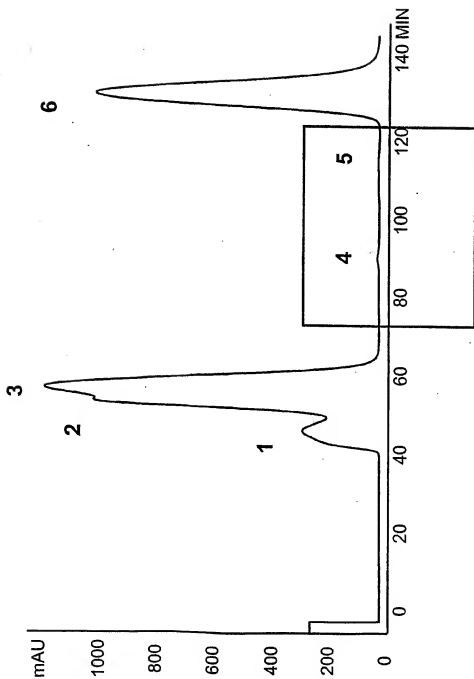


FIG. 172A

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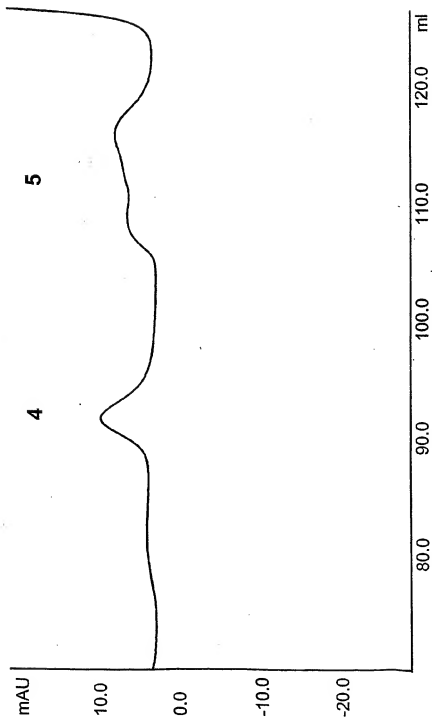


FIG. 172B

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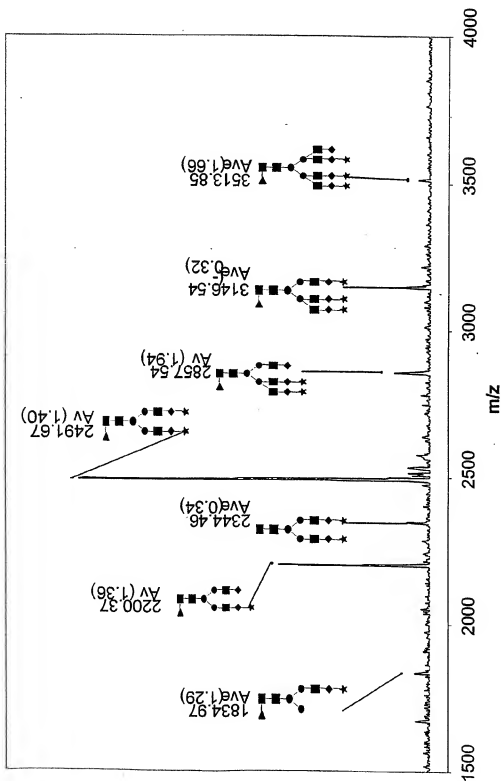


FIG. 173A

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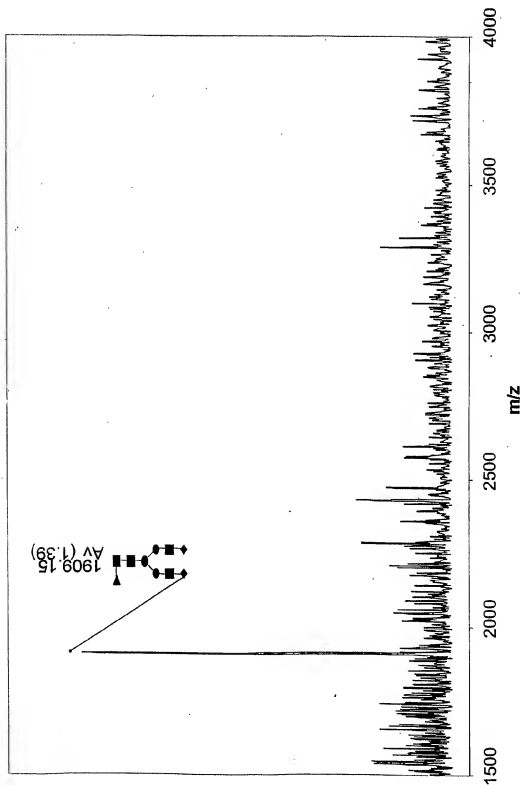


FIG. 173B



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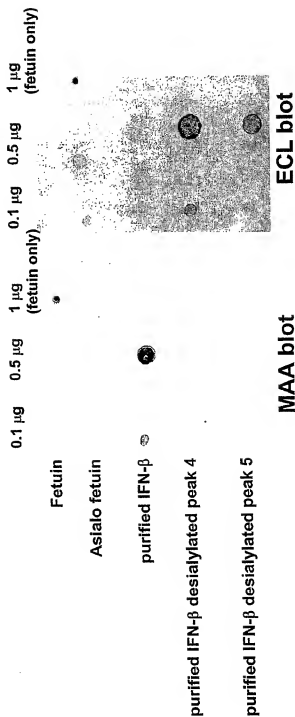


FIG. 174

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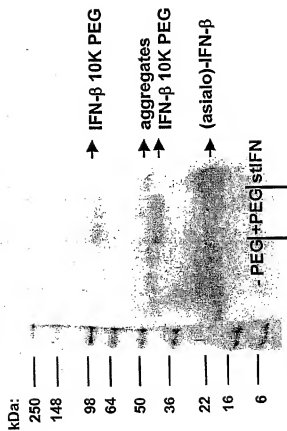
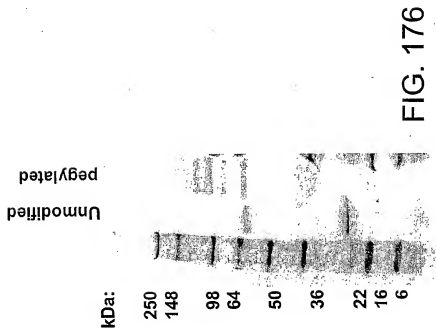


FIG. 175

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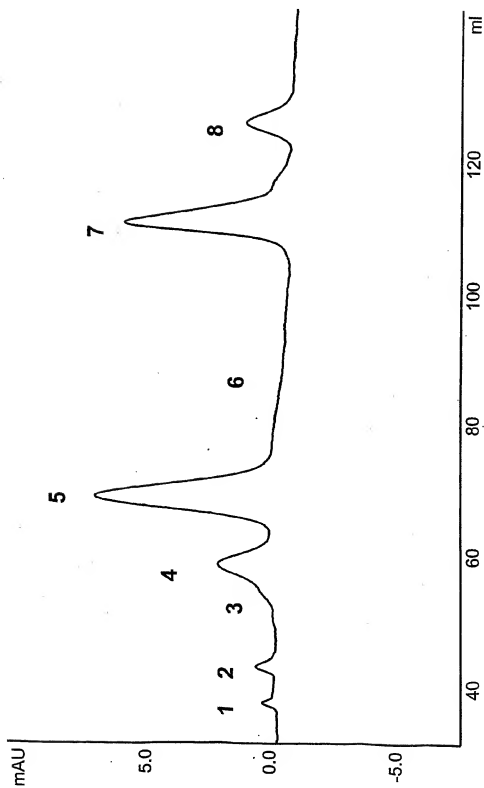


FIG. 177

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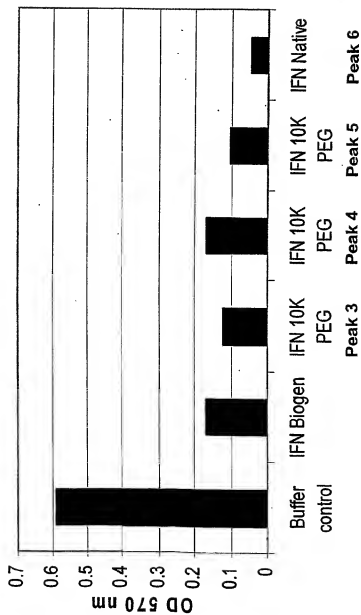


FIG. 178

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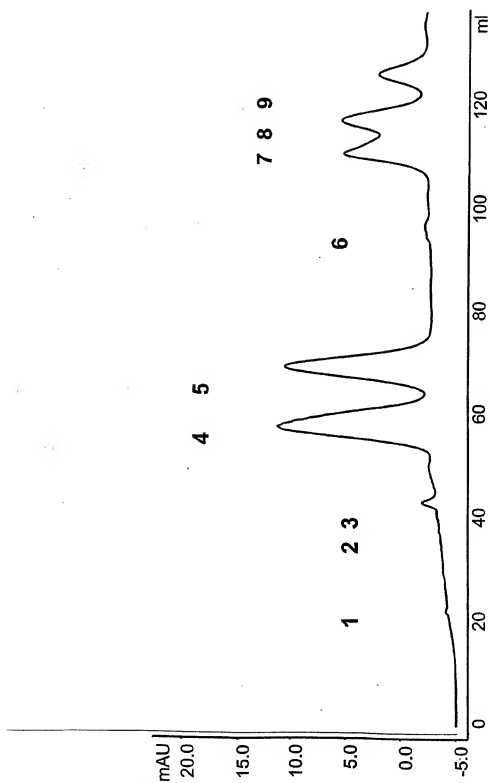


FIG. 179

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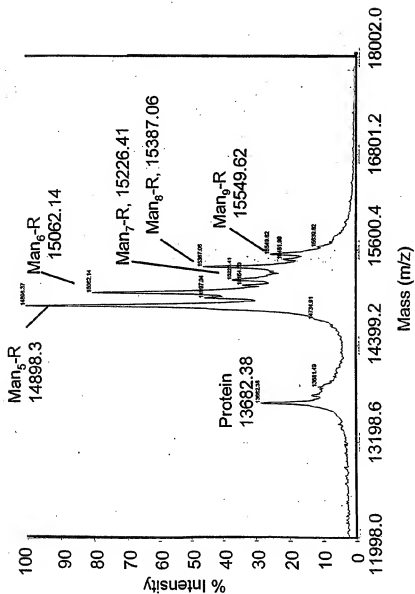


FIG. 180A

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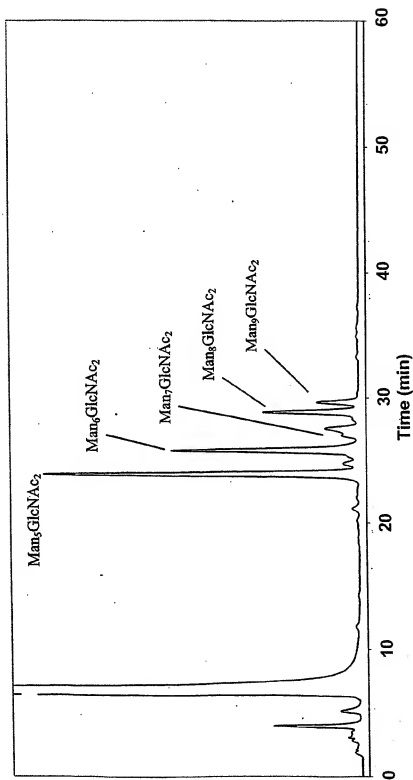


FIG. 180B



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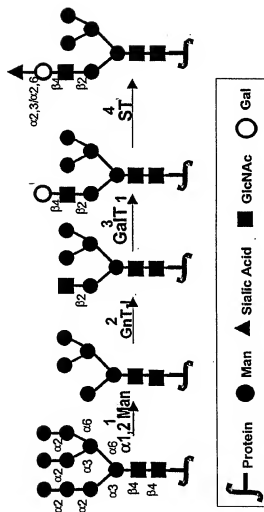


FIG. 181

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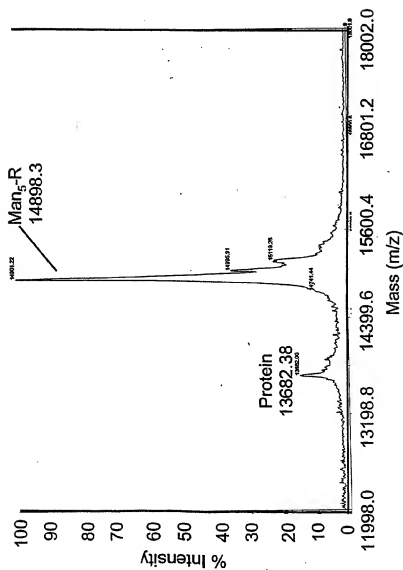


FIG. 182A

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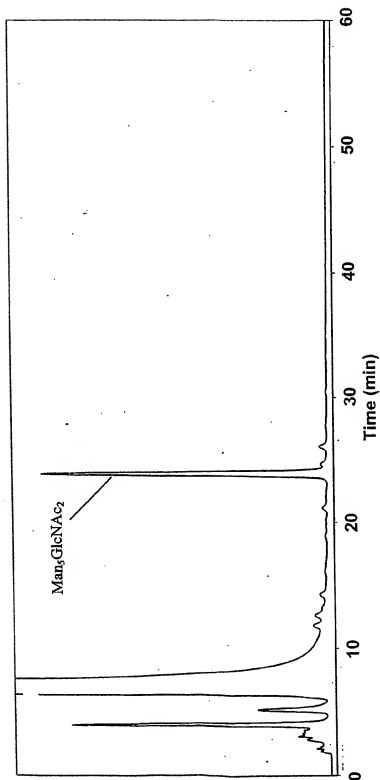


FIG. 182B

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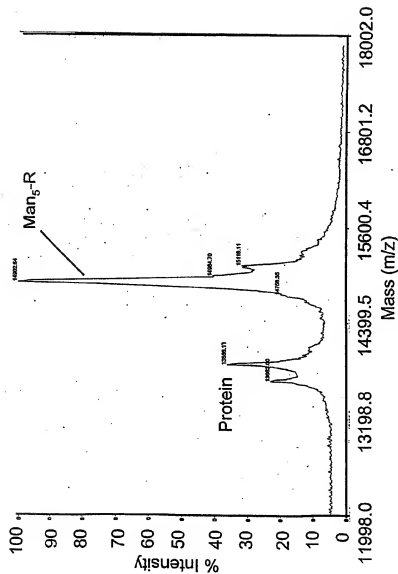


FIG. 183



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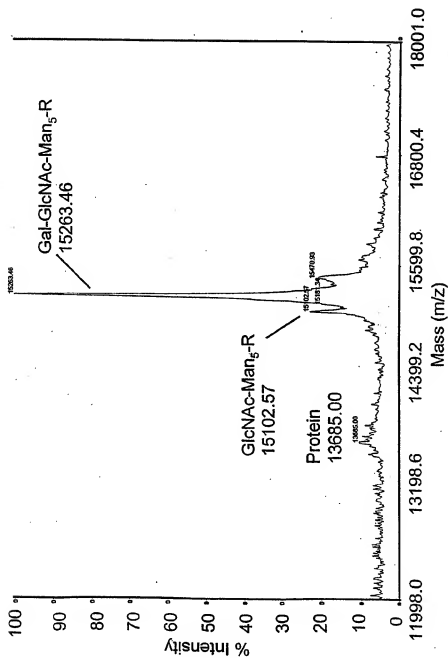


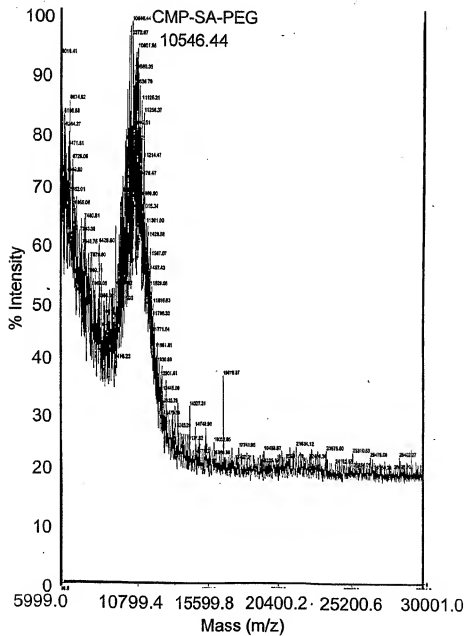
FIG. 185







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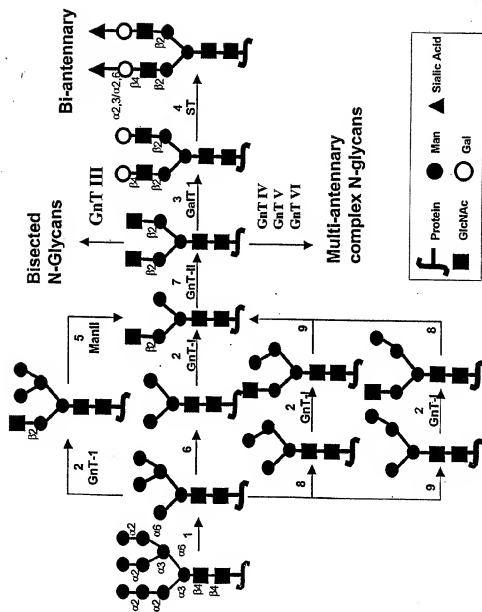


FIG. 188

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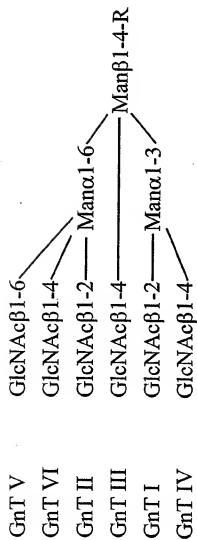


FIG. 189

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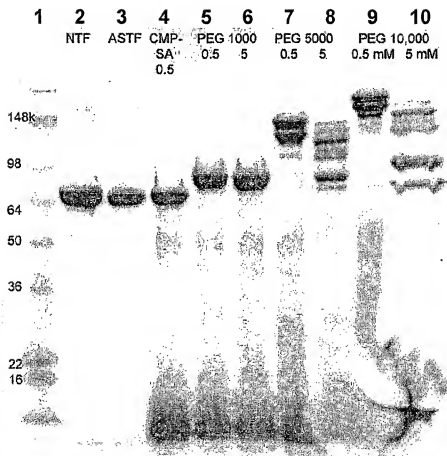


FIG. 190

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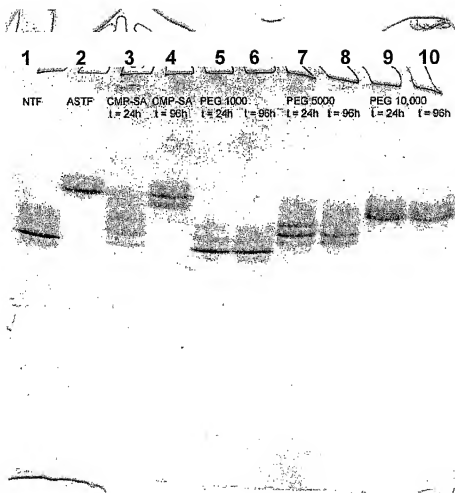
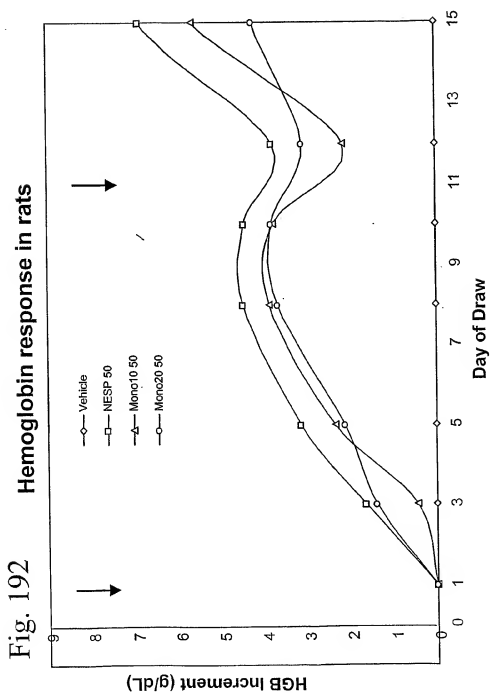


FIG. 191

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## SEQUENCE LISTING

<110> Neose Technologies, Inc.  
 DeFrees, Shawn  
 Zopf, David  
 Bayer, Robert  
 Hakes, David  
 Chen, Xi  
 Bowe, Caryne

<120> ERYTHROPOIETIN: REMODELING AND GLYCOCONJUGATION OF  
 ERYTHROPOIETIN

<130> 040853-01-5083WO

<150> PCT/US02/32263  
 <151> 2002-10-09

<150> US 10/287,994  
 <151> 2002-11-5

<150> US 10/360,770  
 <151> 2003-01-06

<150> US 10/369,779  
 <151> 2003-03-17

<150> US 10/410,945  
 <151> 2003-04-09

<160> 75

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 ctgtgccacc ccgaggagct ggtgctgctc ggacactctc tgggcatccc ctgggctccc 180  
 ctgagcagct gccccagcca ggccctgcag ctggcaggct gcttgagcca actccataga 240  
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 cccaccttgg acacactgca gctggacgtc gccgactttg ccaccacat ctggcagcag 360  
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 gcctctgctt tccagcgccg ggcaggagggt gtcctgggtg cctcccatct gcagagcttc 480  
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<210> 2  
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 <212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

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 1 5 10 15

Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln  
 20 25 30

Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Leu Val  
 35 40 45

Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys  
 50 55 60

Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser  
 65 70 75 80

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser  
 85 90 95

Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp  
 100 105 110

Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro  
 115 120 125

Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe  
 130 135 140

Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe  
 145 150 155 160

Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro  
 165 170

&lt;210&gt; 3

&lt;211&gt; 1733

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

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tcaagttaag taaaatgtca atagcctttt aatttaattt ttaattgttt tatcattcctt 120

tgcaataata aaacattaac ttatatacttt ttaattttaat gtatagaata gagatataca 180

taggatattgt aaatagatac acagtgtata tgtgattaaa atataatggg agattcaatc 240

agaaaaaagt ttctaaaaag gctctgggggt aaaagaggaa ggaacaata atgaaaaaaa 300

tgtggtgaga aaaacagctg aaaacccatg taaagagtgt ataaagaaag caaaaagaga 360

agtagaaaagt aacacagggg catttggaag atgtaaacga gtatgttccc tatttaaggc 420

taggcacaaa gcaaggtctt cagagaacct ggagcctaag gtttaggctc acccatttca 480

accagctctag cagcatctgc aacatctaca atggccttga cctttgcttt actggtggcc 540

ctcctggtgc tcagctgcaa gtcaagctgc tctgtgggct gtgatctgcc tcaaaaccac 600



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caaaaggctg aaaccatccc tgtcctccat gagatgatcc agcagatctt caatctcttc 780
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ctctaccagc agctgaatga cctggaagcc tgtgtgatac aggggggtggg ggtgacagag 900
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ctgggtcaac atggaaatga ttttcattga ttctatgcc agctcacctt tttatgatct 1140
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taaaaataaa cttctgttaa accaagttgt atgtgtgact caagataaca ggtggaacct 1620
aacaataata attctgctct cttgtgtatt tgatttttgt atgaaaaaaa ctaaaaatgg 1680
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<210> 4
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<212> FRT
<213> Homo sapiens

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Lys Ser Ser Cys Ser Val Gly Cys Asp Leu Pro Gln Thr His Ser Leu
20 25 30
Gly Ser Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser
35 40 45
Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu
50 55 60
Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His
65 70 75 80
Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser

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	85		90		95
Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr					
	100		105		110
Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val					
	115		120		125
Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys					
	130		135		140
Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro					
	145		150		155
Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu					
	165		170		175
Ser Thr Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu					
	180		185		

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 <213> Homo sapiens

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 tccatgagct acaacttgct tggattccta caaagaagca gcaattttca gtgtcagaag 120  
 ctctgtggc aattgaatgg gaggttgaa tattgctca aggacaggat gaactttgac 180  
 atcctgagg agattaagca gctgcagcag ttccagaagg aggaagccgc attgaccatc 240  
 tatgagatgc tccagaacat ctttgctatt ttcagacaag attcatctag cactggctgg 300  
 aatgagacta ttgttgagaa cctctggct aatgtctatc atcagataaa ccacttgaag 360  
 acagtctcgg aagaaaaact ggagaaagaa gattttacca ggggaaaact catgagcagt 420  
 ctgcacctga aaagatatta tgggaggatt ctgcattacc tgaaggccaa ggagtacagt 480  
 cactgtgctt ggaccatagt cagagtggaa atcctaagga acttttactt cattaacaga 540  
 cttacaggtt acctcggaaa ctgaagatct cctagcctgt cctctctggga ctggacaatt 600  
 gcttoaagca ttctcaacc agcagatgct gtttaagtga ctgtaggcta atgtactgca 660  
 aatgaaagga cactagaaga ttttgaaatt tttattaaat tatgagttat ttttatttat 720  
 ttaaatttta ttttggaata taaattattt ttggtgc 757

<210> 6  
 <211> 187  
 <212> PRT  
 <213> Homo sapiens

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 20 25 30  
 Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg  
 35 40 45  
 Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu  
 50 55 60  
 Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile  
 65 70 75 80  
 Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser  
 85 90 95  
 Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val  
 100 105 110  
 Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu  
 115 120 125  
 Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys  
 130 135 140  
 Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser  
 145 150 155 160  
 His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr  
 165 170 175  
 Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn  
 180 185

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 <213> Homo sapiens

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 gcgttctcttg aggagctgcg gccgggctcc ctggagaggg agtgcaagga ggagcagtg 180  
 tccttcgagg aggcccgga gatcttcaag gacgcggaga ggacgaagct gttctggatt 240  
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 gaccagctcc agtcttatat ctgcttctgc ctccctgcct tcgagggccg gaactgtgag 360  
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 agtgaccaca cgggcaccaa gcgtcctctgt cggtgccacg aggggtactc tctgtgtgca 480  
 gacggggtgt cctgcacacc cacagttgaa tatccatgtg gaaaaatacc tattctagaa 540  
 aaaagaaatg ccagcaaacc ccaaggccga attgtggggg gcaaggtgtg ccccaaaggg 600  
 gagtgtccat ggcaggtcct gttgttggtg aatggagctc agttgtgtgg ggggaccctg 660

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aacctgatcg cgggtgctggg cgagcacgac ctacgagcgc acgacgggga tgagcagagc 780
cggcgggtgg cgcagggtcat catccccagc acgtacgtcc cgggcaccac caaccacgac 840
atcgcgctgc tccgcctgca ccagcccgtg gtectcactg accatgtggt gccctctgctc 900
ctgcccgaac ggaactgtctc tgagaggacg ctggccttcg tgcgcttctc attggtcagc 960
ggctggggcc agctgctgga cctggcgcc accggccttg agctcatggt gctcaacgtg 1020
ccccgctga tgaccaggga ctgctcgagc cagtcaaggga aggtgggaga ctcccacaaat 1080
atcacggagt acatgttctg tgcgggtac tcggatggca gcaaggactc ctgcaagggg 1140
gacagtggag gccacatgc caccactac cggggcactg ggtacctgac gggcatcgctc 1200
agctggggcc agggctgcgc aaccgtgggc cactttgggg tgtacaccag ggtctccag 1260
tacatcgagt ggctgcaaaa gctcatgccc tcagagccac gccaggaggt cctcctgaga 1320
gccccatttc cc 1332

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<210> 8
<211> 444
<212> PRT
<213> Homo sapiens

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Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val
20 25 30
Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
35 40 45
Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
50 55 60
Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
65 70 75 80
Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
85 90 95
Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
100 105 110
Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
115 120 125
Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
130 135 140
Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
145 150 155 160
Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
165 170 175

```

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val  
 180 185 190  
 Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu  
 195 200 205  
 Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile  
 210 215 220  
 Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg  
 225 230 235 240  
 Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly  
 245 250 255  
 Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr  
 260 265 270  
 Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln  
 275 280 285  
 Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg  
 290 295 300  
 Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser  
 305 310 315 320  
 Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met  
 325 330 335  
 Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser  
 340 345 350  
 Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala  
 355 360 365  
 Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly  
 370 375 380  
 Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val  
 385 390 395 400  
 Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr  
 405 410 415  
 Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu  
 420 425 430  
 Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro  
 435 440

&lt;210&gt; 9

&lt;211&gt; 1437

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 9

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ggatatctac tcaagtctga atgtacagtt ttctctgata atgaaaacgc caacaaaatt 120

ctgaatcggc caaagaggtta taattcaggt aaattggaag agtttgttca agggaaacctt 180  
 gagagagaat gtatggaaga aaagtgtagt tttgaagaac caagagaagt ttttgaaaac 240  
 actgaaaaga caactgaatt ttggaagcag tatgttgatg gagatcagtg tgagtccaat 300  
 ccatgtttaa atggcgccag ttgcaaggat gacattaatt cctatgaatg ttggtgtccc 360  
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 tatogacttg cagaaaacca gaagtctgt gaaccagcag tgccatttcc atgtggaaga 540  
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 tttaatgact tcactcgggt tgttgggtgga gaagatgcca aaccaggcca attcccttgg 720  
 caggttgttt tgaattgtaa agttgatgca ttctgtggag gctctatcgt taatgaaaaa 780  
 tggattgtaa ctgtgcacca ctgtgttgaa actggtgtta aaattacagt tgcgcagggt 840  
 gaacataata ttgaggagac agaacataca gagcaaaagc gaaatgtgat tcgagcaatt 900  
 attcctcacc acaactacaa tgcagctatt aataagtaca accatgacat tgcccctctg 960  
 gaactggagc aaoccttagt gotaaacagc tacgttacac ctatttgcatt tgctgacaag 1020  
 gaatacacga acatcttctc caaatttgga tctggctatg taagtggctg ggcaagagtc 1080  
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 aaatatggaa tatataccaa ggtatccogg tatgtcaact ggattaagga aaaaaccaag 1380  
 ctacctaatt gaaagatgga tttccaaggt taattcattg gaattgaaaa ttaacag 1437

<210> 10  
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 <212> PRT  
 <213> Homo sapiens

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 Ile Cys Leu Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu  
 20 25 30  
 Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn  
 35 40 45  
 Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys

50	55	60
Met Glu Glu Lys Cys Ser Phe Glu Glu Pro Arg Glu Val Phe Glu Asn 65 70 75 80		
Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln 85 90 95		
Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile 100 105 110		
Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys 115 120 125		
Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe 130 135 140		
Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly 145 150 155 160		
Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe 165 170 175		
Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala 180 185 190		
Glu Ala Val Phe Pro Asp Val Asp Tyr Val Asn Pro Thr Glu Ala Glu 195 200 205		
Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser Phe Asn Asp Phe 210 215 220		
Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp 225 230 235 240		
Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile 245 250 255		
Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly 260 265 270		
Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu 275 280 285		
His Thr Glu Gln Lys Arg Asn Val Ile Arg Ala Ile Ile Pro His His 290 295 300		
Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu 305 310 315 320		
Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys 325 330 335		
Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly 340 345 350		
Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu 355 360 365		
Val Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu 370 375 380		

Arg Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe  
385 390 395 400

His Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His  
405 410 415

Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp  
420 425 430

Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val  
435 440 445

Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr  
450 455 460

<210> 11  
<211> 603  
<212> DNA  
<213> Homo sapiens

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ttcttctccc agccgggtgc cccaatactt cagtgcattg gctgctgctt ctctagagca 180  
tatccactc cactaagtc caagaagacg atgttggtcc aaaagaacgt cacctcagag 240  
tcacattgct gtgtagctaa atcatataac agggtcacag taatgggggg tttaaagtgt 300  
gagaaccaca cggcgtgcc ctgcagtact tgttattatc acaaatotta aatgttttac 360  
caagtgcgtt ctgtgatgact gctgattttc tggaatggaa aattaagttg ttagtggtt 420  
atggctttgt gagataaac tctctcttct ctaccatac cactttgaca cgcttcaagg 480  
atatactgca gcttactgc ctctctcctt atctacagc acaatcagca gtctagttct 540  
tttcatttgg aatgaataca gcattaagct tgttccactg caaataaagc cttttaaatc 600  
atc 603

<210> 12  
<211> 116  
<212> PRT  
<213> Homo sapiens

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Val Phe Leu His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro  
20 25 30  
Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro  
35 40 45  
Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro  
50 55 60



Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu  
65 70 75 80

Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly  
85 90 95

Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr  
100 105 110

Tyr His Lys Ser  
115

<210> 13  
<211> 390  
<212> DNA  
<213> Homo sapiens

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<210> 14  
<211> 129  
<212> PRT  
<213> Homo sapiens

<400> 14  
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Cys Cys Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys  
20 25 30  
Glu Glu Cys Arg Phe Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly  
35 40 45  
Tyr Cys Tyr Thr Arg Asp Leu Val Tyr Lys Asp Pro Ala Arg Pro Lys  
50 55 60  
Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val Tyr Glu Thr Val Arg  
65 70 75 80  
Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr Pro Val  
85 90 95  
Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys  
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Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys

115

120

125

Glu

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<210> 15
<211> 1342
<212> DNA
<213> Homo sapiens

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gcccccggtg tggtcacccg gcgcgcacca ggtcgctgag ggaccccggc caggcgcgga 180
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aaaccaccaa aaaaaaaaaa aa 1342

<210> 16
<211> 193
<212> PRT
<213> Homo sapiens

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&lt;400&gt; 16

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Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu  
 20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu  
 35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu  
 50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg  
 65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu  
 85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser  
 100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly  
 115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu  
 130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile  
 145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu  
 165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp  
 180 185 190

Arg

&lt;210&gt; 17

&lt;211&gt; 435

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 17

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 cagggcctgc ggggcagcct caccaagctc aagggccct tgaccatgat gccagccac 300  
 tacaagcagc actgccctcc aaccccgaa acttctgtg caaccagat taccacctt 360  
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ccagtcacagg agtga

435

<210> 18  
 <211> 144  
 <212> PRT  
 <213> Homo sapiens

<400> 18  
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 Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp  
 35 40 45  
 Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe  
 50 55 60  
 Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys  
 65 70 75 80  
 Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met  
 85 90 95  
 Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser  
 100 105 110  
 Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys  
 115 120 125  
 Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu  
 130 135 140

<210> 19  
 <211> 501  
 <212> DNA  
 <213> Homo sapiens

<400> 19  
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 gaggagagtg acagaaaaat aatgcagagc caaattgtct ccttttactt caaacttttt 240  
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 aatgtcaagt ttttcaatag caacaaaaag aaacgagatg acttcgaaaa gctgactaat 360  
 tattcggtaa ctgacttgaa tgtccaacgc aaagcaatac atgaactcat ccaagtgatg 420  
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 <210> 20  
 <211> 166

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 20

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu  
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20 25 30Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn  
35 40 45Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp  
50 55 60Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe  
65 70 75 80Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile  
85 90 95Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg  
100 105 110Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val  
115 120 125Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser  
130 135 140Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg  
145 150 155 160Gly Arg Arg Ala Ser Gln  
165

&lt;210&gt; 21

&lt;211&gt; 1352

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 21

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cctgtgtctgc ctggtccctg tctccctggc tgaggatccc caggagatg ctgccacaga 120

gacagatata tcccaccatg atcaggatca cccaaccttc aacaagatca cccccaacct 180

ggctgagttc gccttcagcc tataccgaca gctggcacac cagtccaaca gcaccaatat 240

cttctctctc ccagtgaagca togctacagc ctttgcaatg ctctccctgg ggaccaaggc 300

tgacaactca gatgaaatcc tggaggggcct gaatttcaac ctacaggaga ttccggaggc 360

tcagatccat gaaggcttcc aggaactcct ccgtaccctc aaccagccag acagccagct 420

ccagctgacc acocggcaatg gcctgttccct cagcgagggc ctgaagctag tggataagtt 480

tttgagggat gttaaaaagt tgtaccacto agaagccttc actgtcaact tcggggacac 540

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<210> 22  
 <211> 418  
 <212> PRT  
 <213> Homo sapiens

<400> 22  
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 Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn  
 35 40 45  
 Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln  
 50 55 60  
 Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser  
 65 70 75 80  
 Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr  
 85 90 95  
 His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro  
 100 105 110  
 Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn  
 115 120 125  
 Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu  
 130 135 140

Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys  
 145 150 155 160  
 Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu  
 165 170 175  
 Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys  
 180 185 190  
 Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu  
 195 200 205  
 Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val  
 210 215 220  
 Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val  
 225 230 235 240  
 Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys  
 245 250 255  
 Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala  
 260 265 270  
 Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu  
 275 280 285  
 Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp  
 290 295 300  
 Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr  
 305 310 315 320  
 Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe  
 325 330 335  
 Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys  
 340 345 350  
 Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly  
 355 360 365  
 Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile  
 370 375 380  
 Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu  
 385 390 395 400  
 Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr  
 405 410 415  
 Gln Lys  
 <210> 23  
 <211> 2004  
 <212> DNA  
 <213> Homo sapiens  
 <400> 23  
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<210> 24  
 <211> 536  
 <212> PRT  
 <213> Homo sapiens

<400> 24  
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 Arg Val Ser Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln  
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 Ala Val Ser Trp Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe  
 35 40 45  
 Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser  
 50 55 60  
 Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu  
 65 70 75 80  
 Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln  
 85 90 95  
 Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln  
 100 105 110  
 Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala  
 115 120 125  
 Ala Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu  
 130 135 140  
 Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val  
 145 150 155 160  
 Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp  
 165 170 175  
 Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp  
 180 185 190  
 Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln  
 195 200 205  
 Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu  
 210 215 220  
 Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro  
 225 230 235 240  
 Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu  
 245 250 255  
 Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu  
 260 265 270

Asn Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu  
275 280 285

Gly Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly  
290 295 300

Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu  
305 310 315 320

Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr  
325 330 335

Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr  
340 345 350

Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg  
355 360 365

Leu Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser  
370 375 380

Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met  
385 390 395 400

Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly  
405 410 415

Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp  
420 425 430

Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp  
435 440 445

Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys  
450 455 460

Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys  
465 470 475 480

Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val  
485 490 495

Val Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys  
500 505 510

Asp Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile  
515 520 525

His Thr Tyr Leu Trp His Arg Gln  
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<210> 25

<211> 1726

<212> DNA

<213> Homo sapiens

<400> 25

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cgacctgac cagggaacacc cgactcctca aaagcaaatg agatcc 1726

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<210> 26  
<211> 562  
<212> PRT  
<213> Homo sapiens  
<400> 26

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 1 5 10 15

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Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg  
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Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys Gln Leu Gln
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Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile
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 Ser Ser Trp Gly Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe  
 980 985 990  
 Lys Gly Lys Arg Ala His Gly Pro Ala Leu Leu Thr Lys Asp Asn Ala  
 995 1000 1005  
 Leu Phe Lys Val Ser Ile Ser Leu Leu Lys Thr Asn Lys Thr Ser  
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 Asn Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp Gly Pro Ser  
 1025 1030 1035  
 Leu Leu Ile Glu Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu  
 1040 1045 1050  
 Ser Asp Thr Glu Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg  
 1055 1060 1065  
 Met Leu Met Asp Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met  
 1070 1075 1080  
 Ser Asn Lys Thr Thr Ser Ser Lys Asn Met Glu Met Val Gln Gln  
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 Lys Lys Glu Gly Pro Ile Pro Pro Asp Ala Gln Asn Pro Asp Met  
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 Ser Phe Phe Lys Met Leu Phe Leu Pro Glu Ser Ala Arg Trp Ile  
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 Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro  
 1130 1135 1140

Ser Pro	Lys Gln	Leu Val	Ser	Leu Gly	Pro Glu	Lys	Ser Val	Glu
1145			1150			1155		
Gly Gln	Asn Phe	Leu Ser	Glu	Lys Asn	Lys Val	Val	Val Gly	Lys
1160			1165			1170		
Gly Glu	Phe Thr	Lys Asp	Val	Gly Leu	Lys Glu	Met	Val Phe	Pro
1175			1180			1185		
Ser Ser	Arg Asn	Leu Phe	Leu	Thr Asn	Leu Asp	Asn	Leu His	Glu
1190			1195			1200		
Asn Asn	Thr His	Asn Gln	Glu	Lys Lys	Ile Gln	Glu	Glu Ile	Glu
1205			1210			1215		
Lys Lys	Glu Thr	Leu Ile	Gln	Glu Asn	Val Val	Leu	Pro Gln	Ile
1220			1225			1230		
His Thr	Val Thr	Gly Thr	Lys	Asn Phe	Met Lys	Asn	Leu Phe	Leu
1235			1240			1245		
Leu Ser	Thr Arg	Gln Asn	Val	Glu Gly	Ser Tyr	Asp	Gly Ala	Tyr
1250			1255			1260		
Ala Pro	Val Leu	Gln Asp	Phe	Arg Ser	Leu Asn	Asp	Ser Thr	Asn
1265			1270			1275		
Arg Thr	Lys Lys	His Thr	Ala	His Phe	Ser Lys	Lys	Gly Glu	Glu
1280			1285			1290		
Glu Asn	Leu Glu	Gly Leu	Gly	Asn Gln	Thr Lys	Gln	Ile Val	Glu
1295			1300			1305		
Lys Tyr	Ala Cys	Thr Thr	Arg	Ile Ser	Pro Asn	Thr	Ser Gln	Gln
1310			1315			1320		
Asn Phe	Val Thr	Gln Arg	Ser	Lys Arg	Ala Leu	Lys	Gln Phe	Arg
1325			1330			1335		
Leu Pro	Leu Glu	Glu Thr	Glu	Leu Glu	Lys Arg	Ile	Ile Val	Asp
1340			1345			1350		
Asp Thr	Ser Thr	Gln Trp	Ser	Lys Asn	Met Lys	His	Leu Thr	Pro
1355			1360			1365		
Ser Thr	Leu Thr	Gln Ile	Asp	Tyr Asn	Glu Lys	Glu	Lys Gly	Ala
1370			1375			1380		
Ile Thr	Gln Ser	Pro Leu	Ser	Asp Cys	Leu Thr	Arg	Ser His	Ser
1385			1390			1395		
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1400			1405			1410		
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1415			1420			1425		
Gln Asp	Asn Ser	Ser His	Leu	Pro Ala	Ala Ser	Tyr	Arg Lys	Lys
1430			1435			1440		
Asp Ser	Gly Val	Gln Glu	Ser	Ser His	Phe Leu	Gln	Gly Ala	Lys

1445	1450	1455
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Val Thr Tyr Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp 1490 1495 1500		
Leu Pro Lys Thr Ser Gly Lys Val Glu Leu Leu Pro Lys Val His 1505 1510 1515		
Ile Tyr Gln Lys Asp Leu Phe Pro Thr Glu Thr Ser Asn Gly Ser 1520 1525 1530		
Pro Gly His Leu Asp Leu Val Glu Gly Ser Leu Leu Gln Gly Thr 1535 1540 1545		
Glu Gly Ala Ile Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys Val 1550 1555 1560		
Pro Phe Leu Arg Val Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser 1565 1570 1575		
Lys Leu Leu Asp Pro Leu Ala Trp Asp Asn His Tyr Gly Thr Gln 1580 1585 1590		
Ile Pro Lys Glu Glu Trp Lys Ser Gln Glu Lys Ser Pro Glu Lys 1595 1600 1605		
Thr Ala Phe Lys Lys Lys Asp Thr Ile Leu Ser Leu Asn Ala Cys 1610 1615 1620		
Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly Gln Asn Lys 1625 1630 1635		
Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr Glu Arg 1640 1645 1650		
Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg His Gln Arg Glu 1655 1660 1665		
Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr 1670 1675 1680		
Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe Asp Ile 1685 1690 1695		
Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys 1700 1705 1710		
Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr 1715 1720 1725		
Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser 1730 1735 1740		
Gly Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr 1745 1750 1755		



Asp Gly	Ser Phe Thr Gln Pro	Leu Tyr Arg Gly Glu	Leu Asn Glu
1760	1765	1770	
His Leu	Gly Leu Leu Gly Pro	Tyr Ile Arg Ala Glu	Val Glu Asp
1775	1780	1785	
Asn Ile	Met Val Thr Phe Arg	Asn Gln Ala Ser Arg	Pro Tyr Ser
1790	1795	1800	
Phe Tyr	Ser Ser Leu Ile Ser	Tyr Glu Glu Asp Gln	Arg Gln Gly
1805	1810	1815	
Ala Glu	Pro Arg Lys Asn Phe	Val Lys Pro Asn Glu	Thr Lys Thr
1820	1825	1830	
Tyr Phe	Trp Lys Val Gln His	His Met Ala Pro Thr	Lys Asp Glu
1835	1840	1845	
Phe Asp	Cys Lys Ala Trp Ala	Tyr Phe Ser Asp Val	Asp Leu Glu
1850	1855	1860	
Lys Asp	Val His Ser Gly Leu	Ile Gly Pro Leu Leu	Val Cys His
1865	1870	1875	
Thr Asn	Thr Leu Asn Pro Ala	His Gly Arg Gln Val	Thr Val Gln
1880	1885	1890	
Glu Phe	Ala Leu Phe Phe Thr	Ile Phe Asp Glu Thr	Lys Ser Trp
1895	1900	1905	
Tyr Phe	Thr Glu Asn Met Glu	Arg Asn Cys Arg Ala	Pro Cys Asn
1910	1915	1920	
Ile Gln	Met Glu Asp Pro Thr	Phe Lys Glu Asn Tyr	Arg Phe His
1925	1930	1935	
Ala Ile	Asn Gly Tyr Ile Met	Asp Thr Leu Pro Gly	Leu Val Met
1940	1945	1950	
Ala Gln	Asp Gln Arg Ile Arg	Trp Tyr Leu Leu Ser	Met Gly Ser
1955	1960	1965	
Asn Glu	Asn Ile His Ser Ile	His Phe Ser Gly His	Val Phe Thr
1970	1975	1980	
Val Arg	Lys Lys Glu Glu Tyr	Lys Met Ala Leu Tyr	Asn Leu Tyr
1985	1990	1995	
Pro Gly	Val Phe Glu Thr Val	Glu Met Leu Pro Ser	Lys Ala Gly
2000	2005	2010	
Ile Trp	Arg Val Glu Cys Leu	Ile Gly Glu His Leu	His Ala Gly
2015	2020	2025	
Met Ser	Thr Leu Phe Leu Val	Tyr Ser Asn Lys Cys	Gln Thr Pro
2030	2035	2040	
Leu Gly	Met Ala Ser Gly His	Ile Arg Asp Phe Gln	Ile Thr Ala
2045	2050	2055	

Ser Gly Gln Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His  
 2060 2070  
 Tyr Ser Gly Ser Ile Asn Ala Trp Ser Thr Lys Glu Pro Phe Ser  
 2075 2080 2085  
 Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile Ile His Gly Ile  
 2090 2095 2100  
 Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser  
 2105 2110 2115  
 Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr  
 2120 2125 2130  
 Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn  
 2135 2140 2145  
 Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn Pro Pro Ile  
 2150 2155 2160  
 Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His Tyr Ser Ile Arg  
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 Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn Ser Cys  
 2180 2185 2190  
 Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln  
 2195 2200 2205  
 Ile Thr Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser  
 2210 2215 2220  
 Pro Ser Lys Ala Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp  
 2225 2230 2235  
 Arg Pro Gln Val Asn Asn Pro Lys Glu Trp Leu Gln Val Asp Phe  
 2240 2245 2250  
 Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln Gly Val Lys  
 2255 2260 2265  
 Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser  
 2270 2275 2280  
 Ser Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys  
 2285 2290 2295  
 Val Lys Val Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val  
 2300 2305 2310  
 Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His  
 2315 2320 2325  
 Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg Met Glu Val Leu  
 2330 2335 2340  
 Gly Cys Glu Ala Gln Asp Leu Tyr  
 2345 2350

&lt;210&gt; 31

&lt;211&gt; 1471

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 31

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1471

&lt;210&gt; 32

&lt;211&gt; 461

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 32

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Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr  
 20 25 30

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln  
 35 40 45

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys  
 50 55 60

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp  
 65 70 75 80

Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys  
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Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg  
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Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu  
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Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg  
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Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val  
 145 150 155 160

Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr  
 165 170 175

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly  
 180 185 190

Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser  
 195 200 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser  
 210 215 220

Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser  
 225 230 235 240

Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly  
 245 250 255

Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly  
 260 265 270

Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys  
 275 280 285

Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro  
 290 295 300

Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu  
 305 310 315 320

Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser

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Ala Leu Asp	Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly					
	340		345		350	
Val Glu Ala	Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser					
	355		360		365	
Asp Ser Ser	Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile					
	370		375		380	
Val Asn Val	Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln					
	385		390		395	
Ala Ser Ser	Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro					
	405		410		415	
Lys Asp Glu	Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser					
	420		425		430	
Gln Leu Glu	Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro					
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Leu Pro Leu	Gly Val Pro Asp Ala Gly Met Lys Pro Ser					
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 <212> DNA  
 <213> Homo sapiens

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 <212> PRT  
 <213> Homo sapiens

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 Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile  
 35 40 45  
 His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile  
 50 55 60  
 Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly  
 65 70 75 80  
 Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser  
 85 90 95  
 Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu  
 100 105 110  
 Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg  
 115 120 125  
 Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln  
 130 135 140  
 Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro  
 145 150 155 160  
 Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg  
 165 170 175  
 Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp

	180		185		190
Phe Ala	Ala Ile Tyr Arg Arg His	Arg Gly Gly Ser Val Thr Tyr Val			
	195	200		205	
Cys Gly	Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His				
	210	215		220	
Cys Phe	Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly				
	225	230		235	240
Arg Ser	Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val				
	245		250		255
Glu Asn	Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His				
	260		265		270
His Asn	Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys				
	275		280		285
Ala Gln	Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr				
	290	295		300	
Asn Asp	Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys				
	305	310		315	320
Glu Asn	Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val				
	325		330		335
Val Lys	Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly				
	340		345		350
Ser Glu	Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys				
	355		360		365
Thr Asp	Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu				
	370		375		380
Gln Gly	Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys				
	385	390		395	400
Ala Leu	Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu				
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Pro Trp	Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu				
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<213>	Mus musculus				
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Val Ala	Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile				
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Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly  
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Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
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<212> PRT  
<213> Mus musculus

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35 40 45

Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
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Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln  
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Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 37  
<211> 120  
<212> PRT  
<213> Mus musculus

<400> 37  
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Gly Met Ser Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu  
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Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser  
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Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val  
 65 70 75 80  
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr  
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 Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala  
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 <211> 106  
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 35 40 45  
 Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser  
 50 55 60  
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp  
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 100 105

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 cattctcgtc atctctgagg acatcaccat catctcagga tgagggggcat gaagctgctg 180  
 ggggcgtgc tggcactggc ggcctactg cagggggccg tgtccctgaa gatcgagcc 240  
 ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccacctcgt cagctacatt 300  
 gtgcagatcc tgagccgcta tgacatcgcc ctgggtccagg aggtcagaga cagccacctg 360  
 actgcctgtg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac 420  
 gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg 480

cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgcga gccctgcggg 540  
 aacgacacct tcaaccgaga gccagccatt gtcaggttct tctccgggtt cacagaggtc, 600  
 agggagtttg ccaattgttc cctgcatgcg gccccggggg acgcagtagc cgagatcgac 660  
 gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttggagga cgtcatgttg 720  
 atgggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtggtc atccatccgc 780  
 ctgtggacaa gcccaccctt ccagtggctg atccccgaca gcgctgacac cacagctaca 840  
 cccagccact gtgcctatga caggatcgtg gttgcagga tgctgctcgg aggcgcggtt 900  
 gttcccgact cggctcttcc cttaacttc caggctgcct atggcctgag tgaccaactg 960  
 gcccaagcca tcagtgacca ctatccagtg gaggtgatgc tgaagtgagc agcccctccc 1020  
 cacaccagtt gaactgcag 1039

<210> 40

<211> 282

<212> PRT

<213> Homo sapiens

<400> 40

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu  
1 5 10 15

Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr  
20 25 30

Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val  
35 40 45

Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp  
50 55 60

Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp  
65 70 75 80

Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn  
85 90 95

Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser  
100 105 110

Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn  
115 120 125

Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe  
130 135 140

Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly  
145 150 155 160

Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val  
165 170 175

Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn  
180 185 190

Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu  
195 200 205

Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr  
210 215 220

Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly  
225 230 235 240

Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn  
245 250 255

Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser  
260 265 270

Asp His Tyr Pro Val Glu Val Met Leu Lys  
275 280

<210> 41  
<211> 678  
<212> DNA  
<213> Mus musculus

<400> 41  
gacatcttgc tgactcagtc tccagccatc ctgtctgtga gtccaggaga aagagtcagt 60  
ttctcttcca gggccagtc gttcgttggc tcaagcatcc actggtatca gcaagaaca 120  
aatggtcttc caagccttct cataaagtat gttcttgagt ctatgtctgg gatcccttc 180  
aggtttagtg gcagtggtgc agggacagat tttactctta gcatcaaac tgtggagtct 240  
gaagatattg cagattatta ctgtcaacaa agtcatagct ggccattcac gttcggctcg 300  
gggacaaatt tggaagtaaa agaagtgaag cttgaggagt ctggaggagg cttggtgcaa 360  
cctggaggat coactgaaact ctctgtgttt gcctctggat tcatittcag taacctctgg 420  
atgaactggg tccgccagtc tccagagaag gggottgagt gggtttgtga aattagatca 480  
aaatctatta attctgcaac acattatgcg gagtctgtga aaggagggtt caccatctca 540  
agagatgatt ccaaaagtgc tgtctacctg caaatgaccg acttaagaac tgaagacact 600  
ggcgtttatt actgttccag gaattactac ggtagtacct acgactactg gggccaaggc 660  
accactctca cagtctcc 678

<210> 42  
<211> 226  
<212> PRT  
<213> Mus musculus

<400> 42  
Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly  
1 5 10 15  
Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser  
20 25 30

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile  
 35 40 45  
 Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser  
 65 70 75 80  
 Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe  
 85 90 95  
 Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu  
 100 105 110  
 Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser  
 115 120 125  
 Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His Trp Met Asn Trp Val  
 130 135 140  
 Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile Arg Ser  
 145 150 155 160  
 Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu Ser Val Lys Gly Arg  
 165 170 175  
 Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr Leu Gln Met  
 180 185 190  
 Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg Asn  
 195 200 205  
 Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr  
 210 215 220

Val Ser  
225

<210> 43  
 <211> 450  
 <212> DNA  
 <213> Homo sapiens

<400> 43  
 gctgcatcag aagaggccat caagcacatc actgtccctc tgccatggcc ctgtggatgc 60  
 gccctctgcc cctgctggcg ctgctggccc tctggggacc tgacccagcc gcagccttgy 120  
 tgaaccaaca cctgtggcgc toacacctgg tggaagetct ctacctagtg tgcgggggaa 180  
 gaggtctctt ctacacaccc aagaccgccg gggaggcaga ggacctgcag gtggggcgag 240  
 tggagctggg cggggggcct ggtgcaggca gccctgcagc cttggccctg gaggggtccc 300  
 tgcagaagcg tggcattgtg gaacaatgct gtaccagcat ctgctccctc taccagctgy 360  
 agaactactg caactagacg cagcccgcag gcagccccc acccgccgcc tctgacacg 420  
 agagagatgg aataaagccc ttgaaccagc 450

<210> 44  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 44  
 Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu  
 1 5 10 15  
 Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly  
 20 25 30  
 Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe  
 35 40 45  
 Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly  
 50 55 60  
 Gln Val Glu Leu Gly Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu  
 65 70 75 80  
 Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys  
 85 90 95  
 Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn  
 100 105 110

<210> 45  
 <211> 1203  
 <212> DNA  
 <213> Hepatitis B virus

<400> 45  
 atgggagggtt ggtcttccaa acctcgacaa ggcattggga cgaatcttct tgttccaat 60  
 cctctgggat tctttccoga tcaccagttg gaccctggt tcggagccaa ctcaacaat 120  
 ccagattggg acttcaacc caacaaggat cactggccag aggcaatcaa ggtaggagcg 180  
 ggagacttcg ggccagggtt caccaccaca caccggcggt ttttggggtg gagccctcag 240  
 gctcagggca tattgacaac agtgccagca gcgcctctct ctgtttccac caatcgccag 300  
 tcaggaagac agcctactcc catctctcca cctctaagag acagtcatcc tcaggccatg 360  
 cagtgaact ccacaacatt ccaccaagct ctgctagatc ccagagttag ggcctatat 420  
 tttcctgctg gtggctccag ttccggaaca gttaaaccctg ttccgactac tgtctcacc 480  
 atatcgtaaa tcttctcgag gactggggac cctgcacoga acatggagag cacaacatca 540  
 ggattcttag gaccctgct cgtgttacag gcgggggttt tcttgttgac aagaatctct 600  
 acaataccac agagtctaga ctggtggttg acttctctca attttctagg gggagcacc 660  
 acgtgtcctg gccaaaattc gcagtcacca acctccaatc actcaccacac ctctgttct 720  
 ccaatttgct ctgggtatcg ctggatgtgt ctgcggcggt ttatcatatt cctcttcac 780  
 ctgctgtat gccctatctt cttgttggtt cttctggact accaaggtag gttgcccggt 840

tgtcctctac ttccaggaac atcaactacc agcacgggac catgcaagac ctgcacgatt 900  
 cctgctcaag gaacctctat gtttccctct tgggtgctga caaaaccttc ggacggaaac 960  
 tgcacttgta ttcccatccc atcactctgg gctttcgcaa gattcctatg ggagtgggcc 1020  
 tcagtcggtt tctcctggct cagtttacta gtgcatttg ttcagtgggt cgcagggctt 1080  
 tccccactg tttggcttcc agttatatgg atgatgtggt attgggggcc aagtcgtac 1140  
 aacatcttga gtcccttttt acctctatta ccaattttct tttgtctttg ggtatacatt 1200  
 tga 1203

<210> 46  
 <211> 400  
 <212> PRT  
 <213> Hepatitis B virus

<400> 46  
 Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu  
 1 5 10 15  
 Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro  
 20 25 30  
 Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn  
 35 40 45  
 Lys Asp His Trp Pro Glu Ala Ile Lys Val Gly Ala Gly Asp Phe Gly  
 50 55 60  
 Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln  
 65 70 75 80  
 Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Val Ser  
 85 90 95  
 Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu  
 100 105 110  
 Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His  
 115 120 125  
 Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly  
 130 135 140  
 Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Val Ser Pro  
 145 150 155 160  
 Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Met Glu  
 165 170 175  
 Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly  
 180 185 190  
 Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser  
 195 200 205  
 Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly  
 210 215 220

Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro  
 225 230 235 240  
 Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile  
 245 250 255  
 Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu  
 260 265 270  
 Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser  
 275 280 285  
 Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly  
 290 295 300  
 Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn  
 305 310 315 320  
 Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu  
 325 330 335  
 Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro  
 340 345 350  
 Phe Val Gln Trp Phe Ala Gly Leu Ser Pro Thr Val Trp Leu Ser Val  
 355 360 365  
 Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser  
 370 375 380  
 Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile  
 385 390 395 400

&lt;210&gt; 47

&lt;211&gt; 799

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 47

cgaaccactc agggctcctgt ggacagctca cctagctgca atggctacag gctcccgga 60  
 gtccctgctc ctggcttttg gctgctctg cctgacctgg cttcaagagg gcagtgacct 120  
 cccaaccatt cccttatcca ggccttttga caacgctatg ctcgcgcgcc atcgtctgca 180  
 ccagctggcc tttagacctt accaggagtt tgaagaagcc tatatcccaa aggaacagaa 240  
 gtattcatct ctgcagaacc ccagacctc cctctgtttc tcagagtcta ttccgacacc 300  
 ctccaacagg gaggaaacac aacagaaatc caacctagag ctgctccgca tctcctgct 360  
 gctcatccag tcgtggctgg agcccgctga gttcctcagg agtgccttcg ccaacagcct 420  
 ggtgtacggc gctctgaca gcaacgtcta tgacctcta aaggacctag aggaaggcat 480  
 ccaaacgctg atggggaggc tggaagatgg cagcccccg actgggcaga tcttcaagca 540  
 gacctacagc aagttcgaca caaactcaca caacgatgac gcactactca agaactacgg 600  
 gctgctctac tgcttcagga aggacatgga caaggtcgag acattcctgc gcagtgtgca 660

gtgccgctct gtggagggca gctgtggctt ctatgtgccc ggggtggcatc cctgtgaccc 720  
 ctcccagtg cctctcctgg ccttggaagt tgccactcca gtgccacca gccctgtcct 780  
 aataaaatta agttgcatc 799

<210> 48  
 <211> 217  
 <212> PRT  
 <213> Homo sapiens

<400> 48  
 Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu  
 1 5 10 15  
 Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu  
 20 25 30  
 Ser Arg Pro Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln  
 35 40 45  
 Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys  
 50 55 60  
 Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe  
 65 70 75 80  
 Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys  
 85 90 95  
 Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp  
 100 105 110  
 Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val  
 115 120 125  
 Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu  
 130 135 140  
 Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg  
 145 150 155 160  
 Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser  
 165 170 175  
 His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe  
 180 185 190  
 Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys  
 195 200 205  
 Arg Ser Val Glu Gly Ser Cys Gly Phe  
 210 215

<210> 49  
 <211> 963  
 <212> DNA  
 <213> Homo sapiens

<400> 49



atggagacag acacactcct gttatgggtg ctgctgctct gggttccagg ttccactggt 60  
gacgtcaggc gagggcccg gagcctgcgg ggcaggggacg cgcacagccc caccgccctgc 120  
gtcccggcgg agtgcttcga cctgctggtc cgccactgog tggcctgcgg gctcctgcgc 180  
acgcccgggc cgaacccggc cggggccagc agccctgcgc ccaggacggc gctgcagccg 240  
caggagtccg tgggcgcggg ggccggcgag gcggcggtcg acaaaactca cacatgccca 300  
ccgtgcccg caccctgaact cctgggggga ccgtcagttc tcctcttccc cccaaaaccc 360  
aaggacaccc tcattgatctc ccggaccctc gaggtcacat gcgtggtggt ggacgtgagc 420  
cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc 480  
aagacaaagc cgcgggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc 540  
gtcctgcacc aggactggct gaatggcaag gactacaagt gcaaggtctc caacaaagcc 600  
ctccagccc ccactcgaga aaccatctcc aaagccaaag ggcagccccg agaaccacag 660  
gtgtacaccc tgcccccac cccggatgag ctgaccaaga accaggtcag cctgacctgc 720  
ctgggtcaaag gctttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg 780  
gagaacaact acaagaccac gcctcccgtg ttggactccg acggctcctt cttcctctac 840  
agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtctcttc atgtccctg 900  
atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tcccgggaaa 960  
tga 963

&lt;210&gt; 50

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 50

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
1 5 10 15

Gly Ser Thr Gly Asp Val Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg  
20 25 30

Asp Ala Pro Ala Pro Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu  
35 40 45

Leu Val Arg His Cys Val Ala Cys Gly Leu Leu Arg Thr Pro Arg Pro  
50 55 60

Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro Arg Thr Ala Leu Gln Pro  
65 70 75 80

Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val Asp Lys Thr  
85 90 95

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser  
100 105 110

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg  
 115 120 125  
 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro  
 130 135 140  
 Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala  
 145 150 155 160  
 Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val  
 165 170 175  
 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr  
 180 185 190  
 Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr  
 195 200 205  
 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
 210 215 220  
 Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys  
 225 230 235 240  
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser  
 245 250 255  
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp  
 260 265 270  
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser  
 275 280 285  
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala  
 290 295 300  
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 305 310 315 320  
 <210> 51  
 <211> 107  
 <212> FRT  
 <213> Homo sapiens  
 <400> 51  
 Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr  
 20 25 30  
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45  
 Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp

85 90 95  
 Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys  
 100 105  
 <210> 52  
 <211> 107  
 <212> PRT  
 <213> Mus musculus  
 <400> 52  
 Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr  
 20 25 30  
 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Ile Val Lys Leu Leu Ile  
 35 40 45  
 Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln  
 65 70 75 80  
 Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp  
 85 90 95  
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
 100 105  
 <210> 53  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens  
 <400> 53  
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
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 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr  
 20 25 30  
 Leu Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile  
 35 40 45  
 Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe  
 50 55 60  
 Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr  
 65 70 75 80  
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys  
 85 90 95  
 Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> 54  
 <211> 119  
 <212> PRT  
 <213> Mus musculus

<400> 54  
 Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Gly Pro Gly Thr  
 1 5 10 15  
 Ser Val Arg Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr  
 20 25 30  
 Leu Ile Glu Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile  
 35 40 45  
 Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe  
 50 55 60  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr  
 65 70 75 80  
 Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys  
 85 90 95  
 Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Arg Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ala  
 115

<210> 55  
 <211> 214  
 <212> PRT  
 <213> Homo sapiens

<400> 55  
 Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr  
 20 25 30  
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45  
 Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp  
 85 90 95  
 Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys Arg Thr Val Ala Ala  
 100 105 110  
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140  
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160  
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
 165 170 175  
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
 180 185 190  
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
 195 200 205  
 Phe Asn Arg Gly Glu Cys  
 210  
 <210> 56  
 <211> 448  
 <212> PRT  
 <213> Homo sapiens  
 <400> 56  
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
 1 5 10 15  
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr  
 20 25 30  
 Leu Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile  
 35 40 45  
 Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe  
 50 55 60  
 Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr  
 65 70 75 80  
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys  
 85 90 95  
 Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe  
 115 120 125  
 Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu  
 130 135 140  
 Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp  
 145 150 155 160  
 Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu  
 165 170 175  
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Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val  
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His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro  
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Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr 580 585 590		
Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser 595 600 605		
Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp 610 615 620		

Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu  
625 630 635 640

Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro  
645 650

<210> 67  
<211> 1290  
<212> DNA  
<213> Homo sapiens

<400> 67  
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ctcgtttcct gggacatccc tggggctaga gcactggaca atggattggc aaggacgcct 120  
accatgggct ggctgcactg ggagcgcttc atgtgcaacc ttgactgccca ggaagagcca 180  
gattcctgca tcagtgagaa gctcttcagt gagatggcag agctcatggt ctcagaaggc 240  
tggaaggatg caggttatga gtacctctgc attgatgact gttggatggc tccccaaga 300  
gattcagaag gcagacttca ggcagaccct cagcgctttc ctcattggat togccagcta 360  
gctaattatg ttacacagca aggactgaag ctagggtatt atgcagatgt tggaaataaa 420  
acctgcgcag gcttccctcg gagttttgga tactacgaca ttgatccca gacctttgct 480  
gactggggag tagatctgct aaaatttgat ggttgttact gtgacagttt ggaaaaattg 540  
gcagatggtt ataagcacat gtccttgccc ctgaatagga ctggcagaag cattgtgtac 600  
tctgtgagt ggcctcttta tatgtggccc ttcaaaagc ccaattatac agaaatccga 660  
cagtactgca atcactggcg aaattttgct gacattgatg attcctggaa aagtataaag 720  
agtatcttgg actggacatc ttttaaccag gagagaattg ttgatgttgc tggaccaggg 780  
ggttggaatg acccagatat gttagtalt ggcaactttg gcctcagctg gaatcagcaa 840  
gtaactcaga tggcctctg ggctatcatg gctgctcctt tattcatgtc taatgacctc 900  
cgacacatca gccctcaagc caaagctctc cttcaggata aggacgtaat tgccatcaat 960  
caggacccct tgggcaagca aggtaccag cttagacagg gagacaactt tgaagtgtgg 1020  
gaacgacctc tctcaggctt agcctgggct gtacttatga taaaccggca ggagattggt 1080  
ggacctcgct cttataccat cgcagtgtct tccctgggta aaggagtggc ctgtaactct 1140  
gcctgttca tcacacagct cctccctgtg aaaaggaagc tagggttcta tgaattgact 1200  
tcaaggttaa gaagtcacat aaatoccaca ggcactgttt tgcttcagct agaaaaatac 1260  
atgcagatgt cattaataa cttacttta 1290

<210> 68  
<211> 429  
<212> PRT  
<213> Homo sapiens



<400> 68  
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 20 25 30  
 Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu  
 35 40 45  
 Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile  
 50 55 60  
 Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly  
 65 70 75 80  
 Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met  
 85 90 95  
 Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg  
 100 105 110  
 Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly  
 115 120 125  
 Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly  
 130 135 140  
 Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala  
 145 150 155 160  
 Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser  
 165 170 175  
 Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn  
 180 185 190  
 Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met  
 195 200 205  
 Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn  
 210 215 220  
 His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys  
 225 230 235 240  
 Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val  
 245 250 255  
 Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn  
 260 265 270  
 Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala  
 275 280 285  
 Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser  
 290 295 300  
 Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn  
 305 310 315 320

Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn  
 325 330 335  
 Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala  
 340 345 350  
 Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala  
 355 360 365  
 Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile  
 370 375 380  
 Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr  
 385 390 395 400  
 Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln  
 405 410 415  
 Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu  
 420 425  
 <210> 69  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens  
 <400> 69  
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 ttcttctccc agcgggtgc ccaatactt cagtgcattg gctgctgctt ctctagagca 180  
 tatcccatc cactaaggtc caagaagacg atgttggtcc aaaagaacgt cacctcagag 240  
 tccacttgct gtgtagctaa atcatataac agggtcacag taatggggggg ttccaaagtg 300  
 gagaaccaca cggcgtgcca ctgcagtact tgttattatc acaaatctta a 351  
 <210> 70  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens  
 <400> 70  
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 Val Phe Leu His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro  
 20 25 30  
 Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro  
 35 40 45  
 Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro  
 50 55 60  
 Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu  
 65 70 75 80

Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly  
 85 95  
 Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr  
 100 105 110

Tyr His Lys Ser  
 115

<210> 71  
 <211> 498  
 <212> DNA  
 <213> Homo sapiens

<400> 71  
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 gagggctgcc ccgtgtgcat caccgtcaac accaccatct gtgcgggcta ctgccccacc 180  
 atgacccgcg tgctgcaggg ggtcctgcgc gccctgcctc aggtgggtgtg caactaccgc 240  
 gatgtgcgct tcgagtcctc ccgggtccct ggctgcccgc gcggcggtgaa ccccggtggtc 300  
 tcctacgcgc tggtctctcag ctgtcaatgt gcaactctgcc gccgcagcac cactgactgc 360  
 ggggggccca aggaccacc cttgacctgt gatgaccccc gcttcaggga ctctctcttc 420  
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 ccgactctcc cacaataa 498

<210> 72  
 <211> 165  
 <212> PRT  
 <213> Homo sapiens

<400> 72  
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 1 5 10 15  
 Gly Thr Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile  
 20 25 30  
 Asn Ala Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr  
 35 40 45  
 Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val  
 50 55 60  
 Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg  
 65 70 75 80  
 Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val  
 85 90 95  
 Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu  
 100 105 110  
 Cys Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu

115 120 T25  
 Thr Cys Asp Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro  
 130 135 140  
 Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr  
 145 150 155 160  
 Pro Ile Leu Pro Gln  
 165

<210> 73  
 <211> 165  
 <212> PRT  
 <213> Homo sapiens

<400> 73  
 Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu  
 1 5 10 15  
 Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His  
 20 25 30  
 Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe  
 35 40 45  
 Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp  
 50 55 60  
 Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu  
 65 70 75 80  
 Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp  
 85 90 95  
 Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu  
 100 105 110  
 Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala  
 115 120 125  
 Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val  
 130 135 140  
 Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala  
 145 150 155 160  
 Cys Arg Thr Gly Asp  
 165

<210> 74  
 <211> 588  
 <212> DNA  
 <213> Homo sapiens

<400> 74  
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 ctgcacaaaa tgaggagaat ctcccctttc ttgtgtctca aggacagaag agacttcagg 180

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ttccccagg agatggtaaa agggagccag ttgcagaagg cccatgtcat gtctgtcctc 240
catgagatgc tgcagcagat cttcagcctc ttccacacag agcgtcctc tgctgcctgg 300
aacatgaccc tcttagacca actccacact ggacttcctc agcaactgca acacctggag 360
acctgcttgc tgcaggtagt gggagaagga gaatctgctg gggcaattag cagccctgca 420
ctgaccttga ggaggtactt ccagggaatc cgtgtctacc tgaagagaa gaaatacagc 480
gactgtgcct gggaagtgtt cagaatggaa atcatgaaat ccttgttctt atcaacaaac 540
atgcaagaaa gactgagaag taaagataga gacctgggct catcttga 588

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<210> 75
<211> 195
<212> PRT
<213> Homo sapiens

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<400> 75
Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr
1 5 10 15

Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu
20 25 30

Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser
35 40 45

Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu
50 55 60

Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu
65 70 75 80

His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
85 90 95

Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu
100 105 110

His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly
115 120 125

Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg
130 135 140

Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser
145 150 155 160

Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe
165 170 175

Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu
180 185 190

Gly Ser Ser
195

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